

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 31, 2003, 21:41:08 ; Search time 76 Seconds
(without alignments)
2102.350 Million cell updates/sec

Title: US-09-857-581-66

Perfect score: 2396

Sequence: 1 MLEELALGLXVLAFLXHLRP.....AHSILVCVPLARIGVASKLLS 521

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents.NA -QFMT=fastp -SUFFIX=p2n.rni -MINWATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents.NA.*

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4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2251	93.9	1824	3	US-08-948-564-13
2	636	26.5	1781	4	US-09-499-302A-1
3	629.5	26.3	1762	3	US-08-881-784-5
4	629.5	26.3	1762	4	US-09-292-768-1
5	629.5	26.3	1762	4	US-09-292-768-65
6	627.5	26.2	1665	3	US-08-881-784-8
7	627.5	26.2	1665	4	US-09-292-768-3
8	627.5	26.2	1665	4	US-09-292-768-67
9	626.5	26.1	1685	4	US-09-292-768-69
10	625	26.1	1806	4	US-09-351-229-3
11	624.5	26.1	1762	4	US-09-292-768-63
12	617.5	25.8	1762	4	US-09-172-339-5

13	611.5	25.5	1515	4	US-09-292-768-5	Sequence 5, Appl
14	590	24.6	1657	3	US-08-948-564-11	Sequence 11, Appl
15	582.5	24.3	2174	3	US-08-606-505B-63	Sequence 63, Appl
16	582.5	24.3	2174	4	US-09-616-390-63	Sequence 63, Appl
17	581.5	24.3	1722	3	US-09-033-055A-1	Sequence 1, Appl
18	577.5	24.1	1665	1	US-08-313-075A-29	Sequence 29, Appl
19	577	24.1	1757	1	US-08-313-075A-49	Sequence 49, Appl
20	575.5	24.0	1927	3	US-08-606-505B-64	Sequence 64, Appl
21	575.5	24.0	1927	4	US-09-616-990-64	Sequence 64, Appl
22	574.5	24.0	1812	1	US-08-313-075A-37	Sequence 37, Appl
23	574.5	24.0	1821	3	US-08-606-505B-1	Sequence 1, Appl
24	574.5	24.0	1824	4	US-09-616-990-1	Sequence 1, Appl
25	572.5	23.9	1893	1	US-08-532-065B-1	Sequence 1, Appl
26	566.5	23.6	1691	3	US-08-948-564-3	Sequence 3, Appl
27	566.5	23.6	2013	4	US-09-615-192A-404	Sequence 404, App
28	564.5	23.6	1634	4	US-09-126-420A-2	Sequence 2, Appl
29	563.5	23.5	1737	4	US-09-126-420A-1	Sequence 1, Appl
30	563.5	23.5	1838	2	US-09-091-432-1	Sequence 1, Appl
31	562.5	23.5	1666	1	US-07-912-900-24	Sequence 24, Appl
32	562.5	23.5	1666	2	US-08-285-309-24	Sequence 24, Appl
33	562.5	23.5	1666	2	US-08-502-046-24	Sequence 24, Appl
34	546.5	22.8	1883	4	US-08-991-677-3	Sequence 3, Appl
35	545.5	22.8	1812	1	US-07-912-900-28	Sequence 28, Appl
36	545.5	22.8	1812	1	US-08-285-309-28	Sequence 28, Appl
37	545.5	22.8	1812	2	US-08-502-046-28	Sequence 28, Appl
38	542.5	22.6	1866	4	US-09-615-192A-103	Sequence 103, App
39	540	22.5	1755	1	US-07-912-900-29	Sequence 29, Appl
40	540	22.5	1755	1	US-08-285-309-29	Sequence 29, Appl
41	540	22.5	1755	2	US-08-502-046-29	Sequence 29, Appl
42	527	22.0	1929	4	US-09-380-420C-1	Sequence 1, Appl
43	522	21.8	1788	3	US-08-948-564-9	Sequence 9, Appl
44	483	20.2	1838	3	US-08-948-564-1	Sequence 1, Appl
45	478	19.9	1698	4	US-09-059-769-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-948-564-13
; Sequence 13, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminszky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1616
US-08-948-564-13

Alignment Scores:
Pred. No.: 4,37e-292 Length: 1824
Score: 2251.00 Matches: 451
Percent Similarity: 86.76% Conservative: 1
Best Local Similarity: 86.56% Mismatches: 69
Query Match: 93.95% Indels: 0
DB: 3 Gaps: 0

US-09-857-581-66 (1-521) x US-08-948-564-13 (1-1824)

Qy 1 MetLeuLeuCluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db 54 ATGTTGCTGACCTGGCTTATGTTGGTCTGTTTCTGCACCTTGGCTCCC 113
Qy 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db 114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAAACCCACCAAGCCAAAGCCT 173
Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuHisTyrAla*** 60
Db 174 CGTCTTCCTTCATAGGACACCTTCATCTCTTAAAGACAAACTTCTCCACTACGCATC 233
Qy 61 IleAspLeuSerLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db 234 ATCGACCTCCCAAAAACATGCTCCCTTATCTCTCTACTTCTGCTCCATGCAACC 293
Qy 81 ValValAlaSerThrProCluLeuPheLysLeuPheLeuGln*****CluAlaThrSer 100
Db 294 GTTGTTCCTCCACACCAAGTTCAGACTCTTCTCCCAACCCAGGAGCACTTCC 353
Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db 354 TTCAACACCAAGTTCACCAACCTTCAGCATAAGACGCTTCACTATAGTACGTGAGCC 413
Qy 121 *****Pro***ClyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
Db 414 ATGGTTCCTTCGGACCTTACTGGAAGTTCGTGAGAAAGCTCATCATGAACGACCTTCC 473
Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db 474 AAGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCCAACACACCGCAAGTTCCTT 533
Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluCluLeuLeu 180
Db 534 AGGGTTATGGCCCAAGGCGCAGGACAGGACAGGACGAGGAGGAGGAGGAGGAGGAGGAGG 593
Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
Db 594 AATGACCAACACAGCACCATCTCCATGATGCTCGGGAGGCTGAGGAGATCAGAC 653
Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db 654 ATCGCTCGGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 713
Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPhe 240
Db 714 TTGACATCTCAGGTTTGAAGATATGAGAGAGATCGACGACATCTTGAACAGTTC 773
Qy 241 AspProValValGluArgValLeuLysLysArgArg***IleValArgArgArg***Asn 260
Db 774 GACCCCTGCTGTAAGAGGTTTCATCAAGAGCGCCCTGAGATCTCGAGGAGGAGAGAAC 833
Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280

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Db 834 GGAGAGGTTTGTGAGGTTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 893
Qy 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
Db 894 GAGGATGAGACCATGAGATCAAAATCAACCAAGGACCATCGAGGTCTGTGTGTGAC 953
Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
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Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
Db 1014 ATCAACAATCTTAAAGTGTGGAAAGGCTCGTGAGGAGGTCTACAGTGTGTGGGAAAG 1073
Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCCTTACATTAGACCAATCGTGA 1133
Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1134 GAGACATTCGCATGTCACCCGCCACTCCCAAGTGTGTCNAAGAAAGTGCACAGAGAGTGT 1193
Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1194 GAGATTATGATATGATGATCCAGAGGAGGAGCATTTGATTTCTTCAATGTATGCAAGTA 1253
Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1254 GGAGACAGCCCAAACTACTGGGACAGACCATCGAGTTCCTCTCTCAGAGGTTCTTAGAG 1313
Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1314 ACAGGGCTGAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1373
Qy 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1374 CCATTTGGTCTGGGAGAGAAATGTGCCCTGGAGTCAATCTGGCTACTTGGGAAATGGCA 1433
Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db 1434 ACATTTCTGATCTCTTATTCAGTGTCTGAGTTCAGTTCAGTGTCTGAGTTCAGTTCAG 1493
Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db 1494 ATATTGAGGTTGGTGAGCCAAAGTTAGCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1553
Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db 1554 AGGCACATAGTCTTGTCTGTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 1613
Qy 521 Ser 521
Db 1614 TCT 1616

RESULT 2
US-09-499-302A-1
; Sequence 1, Application US/09499302A
; Patent No. 6369212
; GENERAL INFORMATION:
; APPLICANT: BOUNG-JUN, OH
; APPLICANT: MOON, KYUNG KO
; APPLICANT: YOUNG, SOON KIM
; TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
; FILE REFERENCE: 10324/P64443USO
; CURRENT APPLICATION NUMBER: US/09/499,302A
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1781
; TYPE: DNA

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ORGANISM: Capsicum annuum
US-09-499-302A-1

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Pred. No.: 636.00 Matches: 153
Score: 49.6% Conservatism: 89
Percent Similarity: 31.42% Mismatches: 209
Best Local Similarity: 26.54% Indels: 36
Query Match: 4 Gaps: 14

US-09-857-581-66 (1-521) x US-09-499-302A-1 (1-1781)

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Qy 53 AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer 72
Dy 157 GGTCCACTTCCTCATCATGGCCTAAATAATCTAGCAAACTTTATGGCCGCTCATGGAC 216
Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
Dy 217 TTACAGCTGGGAAATTCCTACCTCATCATTTCTCCCGCGAATGCGGAAGGAATA 276
Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
Dy 277 CTAAAACTCAGCAC---CTCGCTTCGCCAGCGCGCAAACTTGTGGTGGCTCAGATC 333
Qy 113 LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheVal 131
Dy 334 GTCCATATGATGATGACGATATGATATTTCTCCATATGTTGTAATCTGGAGGAGAT 393
Qy 132 ArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrValAsn***LeuArgProLeu 151
Dy 394 CGTAAATTTGCTACTACTGAACTCTCTAGTGCACAGATGGTCAAAATTTCTTAGCTCAAT 453
Qy 152 ArgThrGlnGlnIleArg-----Lys***LeuArg***MetAlaGln***Aglu 168
Dy 454 CGCCAGGATGAGCTGCTGATGATGCTCATCTATACGAACCATGCCAAATTT----- 507
Qy 169 Ala***LysProLeuAsp***ThrGluGluLeuLysLysTrp***AsnSerThr***Ser 188
Dy 508 -----CCGCTCAACTTACACACAAAATATTTTGTGTTACAGTTCGGTAACCTGT 558
Qy 189 MetMet***LeuGly-----GluAlaGluGluIleArgAspIleAlaArgGlu 204
Dy 559 AGATCAGCTCTGGGAAAAATATGCTGACCAAGACAACTGATAATTTTCATGAGGAA 618
Qy 205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
Dy 619 ATAATATCAATGACAGTGGAATTTAGTATGCTGATTTTCCCTACATGGGAAATGCTA 678
Qy 225 ---LysValGlyLysTyrGlyLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
Dy 679 CATGATGTTGGTGTCTCAAACTAGACGCTCAAGGCTCATCGTAAATCGATGAGATT 738
Qy 244 ValGluArgValIleLysLysArg***IleValArgArg***AsnGlyGlu*** 263
Dy 739 TTGGAACATGATGATGAATGACACAAA-----CAGAATCGAGCGGATGCGCCAAAAG 789
Qy 264 ***GluGlyGlu***SerGlyVal***Leu---AspThrLeuGluPheAlaGluAsp 282
Dy 790 GGTAAATGGGAATTTGGCGTGAAGATTGATCGATGTTTCTAAGGCTTCGAGAAAGT 849
Qy 283 GluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***Phe 302
Dy 850 GGAGAAGTTCAATTTCCATCAGGATGATCAATATCAATCAATATTTAGTGACATGTC 909
Qy 303 SerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsn 322
Dy 910 TCCGCTGGATCTGAACGCTACGACAACTATAATTTGGCCATTTAGTCAAAATGATGAG 969

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Qy 323 AsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp*** 342
Dy 970 AAACCAAGTGTCTAGCAAAAGGACCAAGCTGAAGTGAGCAAGCTCTTGAAGGAAAGAA 1029
Qy 343 LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThr 362
Dy 1030 GGTTCACAAATTTGATCTTGATGAGTGTGAAGTACTTGAAGTAGTAATCAAGAAACT 1089
Qy 363 PheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys*** 381
Dy 1090 CTAAGGATGACCCCTCCATTCCTCTATTAGTCCTAGAGAATCTATGAAGGATACAAAG 1149
Qy 382 IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTTPGlnValGly 401
Dy 1150 ATTACGGGACATAATATACCTTTCAAACTCGAGTCATAGTTAATGATGGCAATTGGA 1209
Qy 402 ***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr 421
Dy 1210 CGAGATCCTGAAAGTTGGGATGACCCCTGAAAGCTTTTCCCCAGAGAGATTC----- 1260
Qy 422 ***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuPro 441
Dy 1261 -----GAGAATAGTCTGTTGACTTTCTTGAAGCCATCATCAATTTATTCGA 1308
Qy 442 PheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThr 461
Dy 1309 TTGCTGCGGAGAGAGATTTGCTCTGGAATGCTTTTGTGTTAGCAATGTTGGACAA 1368
Qy 462 LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIle 481
Dy 1369 CCATAGCTCAATTTACTTTATCATCTGATCGGAAACT-----CCTAATGACAAAGT 1422
Qy 482 LeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArg 501
Dy 1423 CACGAAATTTGGAC-----ATGACGAGTCACTGGAATTTCTGCAACAAGA 1470
Qy 502 AlaHisSerLeuValCysVal 508
Dy 1471 AAGATGATCTTTGTTTGAAT 1491

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RESULT 3

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US-08-881-784-5
; Sequence 5, Application US/08881784
; Patent No. 6083731
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Lupien, Shari L.
; APPLICANT: Kaip, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
; TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; ADDRESS: PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,784
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: WSUR19777
; TELECOMMUNICATION INFORMATION:

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; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Mentha spicata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
US-09-292-768-1

Alignment Scores:
Pred. No.: 1
Score: 1.95e-74
Length: 1762
Percent Similarity: 629.50
Matches: 148
Best Local Similarity: 48.79%
Conservative: 93
Query Match: 29.96%
Mismatches: 212
Indels: 41
Gaps: 14
DB: 4

US-09-857-581-66 (1-521) x US-09-292-768-1 (1-1762)

QY 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
DB 101 TCGAATCCCAACAACTA-----CCTCGAGCCCT---CCGAGCTGCCGTGATC 151
QY 46 GlyHis***HisLeuLysAspLysLeuHisTyrAla***IleAspLeuSerLys 65
DB 152 GGCACCTCCACTCTCTGGGAGGCTTCCCGAGCAGCTGTTTAGGAGCATAGCCAG 211
QY 66 LysHisGlyProLeuPheSer***PheGlySerMetProThrValValAlaSerThr 85
DB 212 AAGTACGGCGCGTGGCCACCTGACGCTGGGAGAGTACTCGGTGGTCTCGTCTG 271
QY 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
DB 272 GCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 328
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
DB 329 GAGGATCGGGTCCAGGACCATGGTACGACAAAGATGATCATCTTCAGCCCTAC 388
QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
DB 389 AACGATCACTGGCGCCAGATCGGAGGATCTGCTGACAGAGCTGCTGAGCCCGAGAAC 448
QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
DB 449 GTCAGTCTCTCGGTACATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 508
QY 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
DB 509 TCGTGGGGGAGCG-----CGGTGACGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
QY 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
DB 563 GTCGTGTGTGACGGCGCGCTCGGAGTGTCTCAAGGACCGAGGAGGAGGAGGAGGAG 622
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
DB 623 TTGTGTAGAGGAGTCCGTGCGCATTCGCGTCCGGTTCGAGCTGGCGGAT---CTCACCT 679
QY 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
DB 680 TCCTCATGGCTCCCTCAACCTGCTAGCTTGAACAAGTAC-----AGGTTGACAGGATG 733
QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
DB 734 CCGCGCGCTCGATCATCATCTCTGATGGGTCTCTGGAGGAGCATAGG----- 781

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RESULT 5

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US-09-292-768-65
; Sequence 65, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croleau, Rodney B
; APPLICANT: Croleau, Rodney B
; APPLICANT: Lapien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; TITLE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

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QY 257 ArgArg***AsnGlyGlu*****GluGlyVal***SerGlyVal***Leu---AspThr 275
DB 782 -----GAGAGAAGACGCGGCACTTTGGAGCGAGACATCTCGTGGAGTT 826
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys 295
DB 827 CTTTTCAGGATGCAAGAGGCGAGCATCAAAATTCCTTCCATTAATTCATCAAG 886
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTyr 315
DB 887 GGTTCATTTTCACACCTCTCCGCGGAGCTGAAACGCTCTTCGAGCACCATCTCATGG 946
QY 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
DB 947 GCGTGTCTGCACTGATGAGGAATCCGCGGAGAGTGCACCAAGTGCAGCGGAGGTAAGA 1006
QY 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
DB 1007 GAGCGCTCAAGGAAAGACAGCTGCTGATTTGAGCGAGGTGCAAGAGCTAAATACCTG 1066
QY 356 ArgAlaIleValLysGluThrPheArgMetHisProLeuProValValLysArgLys 375
DB 1067 AGATCGGTGTTAAAGAGACTCTGAGGCTGCACCTCCCTTTCCATTAATCCCAAGACAA 1126
QY 376 Cys***GluLysCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
DB 1127 TCAGGAGAAGATCGGAGTTAACGGGTACAGATTCCTCGGCCAAACTAGAAATCTTCATC 1186
QY 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
DB 1187 AACGTCTGGCTATCGGAAGGATCCCAATACTACTGGGAAGATCCGACACCTCCGCT 1246
QY 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
DB 1247 GAGAGATTCGATGAGGTTCAGG-----GATTTCATGGGAAC 1285
QY 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
DB 1286 GATTCGAGTTCATCCATTCGCGGCGGTGCAAGAAATGCCCCGGTTTACATTCGGG 1345
QY 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
DB 1346 CTGCGAAATGTTGAGATCCCATTCGCGCAACTGCTTACCACCTTCGACTGGAATG--- 1402
QY 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
DB 1403 ---CCACAGGAATG-----ACTGATGCGGACTTGGACATGACGAGAGCCCCA 1447
QY 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
DB 1448 GGTCTTTCTGGGCCAAAGAAATGTTTGTCTGTTCC 1489

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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1762)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: spearmint limonene-6-hydroxylase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
US-09-292-768-65

Alignment Scores:
Pred. No.: 1,95e-74 Length: 1762
Score: 629.50 Matches: 148
Percent Similarity: 48.79% Conservative: 93
Best Local Similarity: 29.96% Mismatches: 212
Query Match: 26.27% Indels: 41
DB: 4 Gaps: 14

US-09-857-581-66 (1-521) x US-09-292-768-65 (1-1762)
QY 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheile 45
DB 101 TCGAATCCCAACAACTA-----CTCGAGCCCT---CCGAAGCTGCCGGTATC 151
QY 46 GlyHis***HisLeuLeuLysAspLysLeuHisTyrAla***IleAspLeuSerLys 65
DB 152 GCCACCTCCACTTCTGCGGAGGGCTCCCAAGCAGCTGTTAGGAGCATAGCCAG 211
QY 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
DB 212 AAGTACGGCGCGTGGCCACCTGCGAGTGGAGAGTACTCGTGGTCTGCTGCG 271
QY 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
DB 272 GCGGAGGCGCAGCAGCAGCGATGAAGTGTGGAC---CCGAAGCTCGCGCAGCGGTC 328
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
DB 329 GACGCGATCGGTCGACGACCATGTTGACCAAGATGAGATCACTTCAGCCCTTAC 388
QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThr 144
DB 389 AACGATCACTGCGCCAGATCGGAGGATCGCGTACAGAGCTGCTGAGCCCGAAGAC 448
QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
DB 449 GTACAGTCTTGGGTATACATAGGCGAGGAGATCGAGCGCCTCATCCGCTGCTCGG 508
QY 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
DB 509 TCGTGGGGGAGCG-----CCGTCGACGTGACGAGGAGGTGTCGAAGATGCTGCT 562
QY 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
DB 563 GTCTGCTGTGTCAGGCGCGGTTCGGAGTGTGTCAAGACCCAGCGGTTCGTTGGCGG 622
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheile***Pro 220
DB 623 TTGGTGAAGGAGTCTGCTGCAITGCGTCCGGGTTTGAGCTGGCGGAT---CTTACCT 679
QY 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspile 236
DB 680 TCCATGATGCTCCTCAACCTGCTAGCTTGAACAAAGTAC-----AGGTTGACAGGATG 733
QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
DB 734 CCGCCCGCGCTCGATCAGCTCTTGTGTTGAGGAGGATAGG----- 781
QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu--AspThr 275

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DB 782 -----CAGAGAGAGCGCGGAGTTTGGAGCGCAGGACATCTCGACGTT 826
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys 295
DB 827 CTTTTCAGGATGAGAGAGCGCAGCAGCATCAAAATTCCTACTTCCAAATGTCATCAAG 886
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTyr 315
DB 887 GGTTCATTTTCGACACCTTCTCCGGGGAGCGTGAACGCTTTCGACGACCATCTCATGG 946
QY 316 AlaLeuAlaGluLeuLeuAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
DB 947 GCGTCTGCGAAGTATGAGGAATCCGGGAGAGTCCCAAGTGGCGGAGGAGTGAAGA 1006
QY 336 SerValValGlyLysAsp***LeuValAspGluValAlaThrGlnAsnLeuProTyrIle 355
DB 1007 GAGCGCTCAAGGAAAGACAGTCGTGGATTTCGAGGAGGTGCAAGAGTAAATACCTG 1066
QY 356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
DB 1067 AGATCGGTGTTAAAGGAGACTCTGAGGCTGCACCTCCCTTTCCATTAATCCAGACAA 1126
QY 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
DB 1127 TCAGGGAAGATGCGAGGTACAGGATTCGCGCCAAACTAGAAATCTTCATC 1186
QY 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
DB 1187 AAGCTCTGGCTATCGAGAGGATCCCAATACTGGAAGATCCGACACCTTCGCCCT 1246
QY 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
DB 1247 GAGAGATCGATGAGGTTCGAGG-----GATTTCATGGGAAC 1285
QY 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
DB 1286 GATTTCGAGTTTATCCATTCGCGGGGTCGAAGAATCTGCCCGGTTTACATTCGGG 1345
QY 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
DB 1346 CTGCAATTTGAGATCCCATTTGGCGCACTGCTACCATTCGACTTCGACTGGAAATG--- 1402
QY 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
DB 1403 ---CCACAGGAATG-----ACTGATGCGGACTTGGACATGACGAGAGACCCCA 1447
QY 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
DB 1448 GGTCTTCTGGGCCAAAAGAAAATGTTGCTGCTGCC 1489

RESULT 6
US-08-881-784-8
; Sequence 8, Application US/08881784
; Patent No. 6083731
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Lupien, Shari L.
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
; THE PRODUCTION OF LIMONENE HYDROXYLASES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; ADDRESSEE: PLLC
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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FILE REFERENCE: wsr13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1665
TYPE: DNA
ORGANISM: Mentha piperita
FEATURE:
NAME/KEY: CDS
LOCATION: (19)..(1518)
US-09-292-768-3

Alignment Scores:
Pred. No.: 3,33e-74 Length: 1665
Score: 627.50 Matches: 147
Percent Similarity: 48.1% Conservative: 90
Best Local Similarity: 29.88% Mismatches: 204
Query Match: 26.19% Indels: 51
DB: 4 Gaps: 11

US-09-857-581-66 (1-521) x US-09-292-768-3 (1-1665)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 124 CTTCCGGGCCCG---CCGAAGCTCGCTGATCGGGCCACCTCCACCTCTATGGGGAAAG 180
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
DB 181 CTTCCGGCCAGCAGCGCTGCCAGCTGCGGAAGCAGTACGGCCCGCCAGTGGCCCGCCAG 240
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLeuLeuGln 94
DB 241 CTTCCGGCAGGTTCTTCCGCTGCTGCTCGTCCCGCAGGCGCCAGGAGCGCATGAAG 300
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 301 CTTGTGGAC---CCGGCTCGCGCGGCGGCTTCAGAGCATCGGACGACGATCATGTGG 357
QY 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 358 TACGACACGAGGACATCATCTTACGCCCTTACAGCGTCCACGCTGCGGCGCAGCATCGGAAG 417
QY 134 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 418 ATCTCGGCTCGAGACTCTCTCAGCGCCGCGACGCTCCGCTCCTTCGGCTTCATCAGCAG 477
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 478 GACGAGGTCTCCGCTCTCCGCGCACCTCCGCTCTCCGCGCGCGCGGCGGCGGCGGTG 537
QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 538 GACCTCAGGCGGATAGCAGCGCTGACGCTGCTCCATCATCTCAGCGCGCGGCTTCGGG 597
QY 194 -----GluAlaGluLulleArgAspIleAlaArgGluValLeuLysIle*** 209
DB 598 ACGGTGATCAGGACACGAGGAGTGTGTGAGCTGTGTAAGAGCAGCGCTCAGCATGCGG 657
QY 210 GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
DB 658 TCCGGTTCGAGCTCGCGGACATGTTCCCTCCCTCCAGCTCCTCACTTCTCTGTGG 717
QY 225 -----LysValGlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAsp 241
DB 718 AACAGACGACAGCTGTGGAGTATGCGCGCGCTGCGGCGGCGGCGGCGGCGGCGGCGG 774
QY 242 ProValValGluArgValIleLysLysArg***IleValArgArg***AsnGly 261
DB 775 ---GTGGAGGACACAGCTCAAGAG----- 798

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QY 262 Glu*****GluGlyGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
DB 799 -----AGCGCGAGTTTGGCGGAGGACATTAATGACGACTCTTTAGGATGCAG 849
QY 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
DB 850 AAGGATAGCCAGATCAAGTCCCATCACCACCAAGCCATCAAGCCCTTCCTTCGAC 909
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrCluTrpAlaLeuAlaGluLeu 320
DB 910 ACGTTCTCAGCGGAGCGGAGACATCAACACCACCCCTGTGGGTGATGCGGAGCTG 969
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 970 ATGAGGAATCCAGAGGTGATGGCGAAGCGGAGGAGTGCAGACGCGCTGAAGGGG 1029
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1030 AAGACGAGCTGGGAGCGTGGAGCAGCGTGAAGCGGAGTTCATGATCAATCGGTGTGAAG 1089
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
DB 1090 GAGCAGATGAGGATGACCCCTCCGATCCGCTTGCATCCGAGATCATGCGAGAGAATGC 1149
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
DB 1150 GAGGTCAACGGGTACACGATTCGGAATAAGCGGAGTTCATGATCAATCGGTGTGCATG 1209
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1210 GTTAGGATCTCTCTACTCTGGGAAACCCGAGACCTTTTGGCCCGAAGGTTT----- 1263
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1264 -----GACCAAGTCTCGAGGATTTTCATGCGAAGCATTCGAGTTTCATC 1308
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1309 CCATTGGAGCTGGAAGAGAACTCCCGCGGTTGAATTCGGGTGGCAATGTTGAG 1368
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
DB 1369 GTCCCATTTGCGACAGCTTCTTTTACCACTTCGACTGGAAGTTGGCGGAGGAATGACCT 1428
QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
DB 1429 -----TCGATATGACATGTCTGAGCGCAGAGGCCCTT 1461
QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
DB 1462 ACCGGAATAAGAAAGAACAACTCTCTACTCGTTCC 1497

RESULT 8
US-09-292-768-67
Sequence 67, Application US/09292768
Patent No. 6194185
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
FILE REFERENCE: wsr13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 67
LENGTH: 1665
TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-3-hydroxylase
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1665)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-3-hydroxylase variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
US-09-292-768-67

Alignment Scores:
Pred. No.:      3,33e-74      Length:      1665
Score:          627.50      Matches:      147
Percent Similarity: 48.17%      Conservative: 90
Best Local Similarity: 29.88%      Mismatches: 204
Query Match:      26.19%      Indels:      51
DB:              4          Gaps:      11

US-09-857-581-66 (1-521) x US-09-292-768-67 (1-1665)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 124 CTTCCGGGGCCG---CCGAAGTGGCGGTGATCGGGCACCTCCACCTCTATGGGGGAG 180
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuProPheSer**** 74
Db 181 CTGCGCCACACGCGTCCGACGCGGGGAAGACAGTACGGGCCAGTGGCCACGTGCAG 240
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 241 CTCGCGGAGGTCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db 301 CTGGTGGAC---CCGGCTGCGGACCGTTCGAGACGATCGGACGACGATCAATGTTGG 357
QY 115 TyrAsp-----ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 358 TAGCACACGAGGACATCATCTTCAGCCCTCAGCGCTGCACTGGCGCCAGATGGCGAAG 417
QY 134 LeuIleMetAsnAspLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGCTCTCGAGCTCTCAGCCGCCACAGCTCGCTCTCGCTCTCGCTCTCATCAGGCG 477
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTCTCCGCTCTCGCCACCTCCGCTCTCGCCGCGCGCGGGGAGCGCCGTG 537
QY 174 Asp***ThrGluLeuLeuLysTyr***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGCGAGGATACGACGCGTCTCCATCATCTGACGCGCGCGGTTCGCG 597
QY 194 -----GluAlaGluLeuIleArgAspIleAlaArgGluValLeuLysIle*** 209
Db 598 AGCGTGATCAGGACACGAGGAGGTGGTGAGCTGGTCAAGGACGCGCTCAGATGCGG 657
QY 210 GlyGlyTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 658 TCGGGTTCGAGCTCGCCGACATGTTCCTCTCTCCAGCTCTCAAGTGTCTGTCTGCTGG 717
QY 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
Db 718 ACACAGCAGCAGCTGTGGAGGTGGCGCGCGCGCTCGACGCCATCTCTGAGGCCATC--- 774
QY 242 ProValValGluArgValIleLysLysArgArg***IleValArgArg***AsnGly 261
Db 775 ---GTGGAGGAGCACAAAGCTCAAGAAG----- 798

```

```

QY 262 Glu*****GluGlyGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
Db 799 -----ACCGCGAGTTTGGCGGAGACACATTATTGACGTACTCTTTAGGATCAG 849
QY 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
Db 850 AAGGATAGCCAGATCAAGTCCCATCACCACCAAGCCATCAAGCCATCAAGCCATCTTCGAC 909
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db 910 ACGTTCAGCGGGGACCGAGACATCAACACCACCTGCTGGGTGATGGGGAGCTG 969
QY 321 IleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLys 340
Db 970 ATGAGGAATCCAGAGGTGATGTCGCGAAAGCGCAGCGGAGTGCAGAGCGGCTGAAGGG 1029
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACGCGACTGGGACGTGGACGCTGACGAGGCTTAAGTACATGAATCGGTGGTGAAG 1089
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db 1090 GAGACGATGAGGATGCACCTCCGATCCGCTGATCCCGAGATCATGCAGAGAAGATGC 1149
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGTCAACGGGTACACGATTCGGAATAGCCAGATCATGATCAACGCTGCTGCTCATG 1209
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GTAGGATCTCTCTACTGCGAAACCGGAGACCTTTTGGCCCGAAGGTTT----- 1263
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1264 -----GACCAAGTCTCGAGGATTCATGGAACGATTTTCGAGTTTCATC 1308
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db 1309 CCATTTCGAGCTGAAGAGAAATCTGCCCGTTTGAATTCGGGTGGCAATGTTTCAG 1368
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db 1369 GTCCCATTCGCGACAGCTCTTACACTTCGACTGGAAGTTGGCGGAAGGAATGAACCT 1428
QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
Db 1429 -----TCCGATATGGACATGTCTGAGGACGAAGGCTT 1461
QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAAGAAAGAACAACTCTTCTACTGTTCCC 1497

RESULT 9
US-09-292-768-69
; Sequence 69, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: WSUR13463
; CURRENT APPLICATION NUMBER: US/09/292.768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881.784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

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799 Db -----ACGGCGCACTTTGGCGCGAGGACATTATTGACGCTACCTCTTAGGATCGAG 849
281 Qy GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp 300
850 Db AAGGATAGCCAGATCAAGTCCCATCATCCACCACGCCATCAAGCGCTTCATCTTCGAC 909
301 Qy ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
910 Db ACGTTCACGCGGGGAGAGACATCAACACCACCTGTGGGTGATGGCGGACGCTG 969
321 Qy IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
970 Db ATGAGGAATCCAGAGGTGATGGCGAAAGCCAGCGGAGTGAGAGCGCGCTCAAGGG 1029
341 Qy Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
1030 Db AAGACGGACTGGGACGTGGACGCTGCAGAGCTTAAGTACATGAATCGGTGGTGAG 1089
361 Qy GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
1090 Db GAGACGATGAGGATGCACCTCCGATCCGCTTGATCCGAGATCATCCAGAGAAGATGC 1149
381 Qy ***IleAsnGly***Val***ProGluGluAlaLeu*****PheAsnValTrpGlnVal 400
1150 Db GAGTCAACGGGTACACGATCCGATTAAGGCCAGAAATCATGATCAAGTGTGGTCCATG 1209
401 Qy Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
1210 Db GGTAGGAATCCTCTCTACTGTGGAAAAACCGAGACCTTTTGGCCGAAAGGTTT----- 1263
421 Qy Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
1264 Db -----GACCAAGTCTCAGGAGTTTCATGGGAACAGATTTCGAGTTCATC 1308
441 Qy ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
1309 Db CCATTTGCGAGCTGGAAGAGAATCTGCCCGGTTTGAATTTCCGGTTTGGCAAAATGTTGAG 1368
461 Qy ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
1369 Db GTCCCATGGCCAGACTTCATTACCACCTTCGACTGGAAGTTGGCGGAGGAATGAACCT 1428
478 Qy GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeu 497
1429 Db -----TCCGATATGGACATGTCTGAGGCGAAGGCGCTT 1461
498 Qy ThrValProArgAlaHisSerLeuValCysValPro 509
1462 Db ACCGGAATAGAAGACATCTTCTACTCGTTCC 1497

RESULT 10
US-09-351-229-3
; Sequence 3, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Zea mays
US-09-351-229-3
Alignment Scores:

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Pred. No.: 8.14e-74 Length: 1806
Score: 625.00 Matches: 165
Percent Similarity: 50.60% Conservative: 90
Best Local Similarity: 32.74% Mismatches: 198
Query Match: 26.09% Indels: 52
DB: 4 Gaps: 13

US-09-857-581-66 (1-521) x US-09-351-229-3 (1-1806)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 86 CGCGCGGCCCCAAGCCA---TGGCGGATCATCGGCAACCTTAACCTCATG---GGCGAG 139
QY 55 LeuLeuHisThrAla***IleAspLeuSerLysHisGlyProLeuPheSer***** 74
DB 140 CTGCCCCACCGCTCCATGAACAGAGCTCTCAAGCGGTACGGTCCCTCATGAGCTCTGG 199
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
DB 200 TTGCGGTCTGTCCTGTTGCTGCGCGGTCCGCGAGATGGCAAGCTCTTCTCTCAAG 259
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 260 ACCAAGCAGCG---CGCTTCCGACCGCGCGAGGTTTCGAGTCGCGAAGTACACCGCG 316
QY 115 ThrAsp-*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 317 TAGGACTGCTCGCGCTCTGTCGCTCTGTCGCTCTTTTGGCGGTACCTCGCGCAGCGCAGG 376
QY 134 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 377 ATCTGCGCCACCGAGCTCTCAGCGCCAGCGCGCTCGAGTCTTCGACGACATCCGCGAC 436
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 437 GAGGAGTCCGCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496
QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 497 AGGGACTACTCGAGATGTG-----GGGCTCGCGGTGATCTCGGATAGTCTTCTGGGC 550
QY 194 Glu----- 194
DB 551 AAGAGTAGTGTATGAGGAGCGCGGAGCGGTGAGGGGAGCTCAGCGCGCGGATAACG 610
QY 195 AlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyLeuTyrSerLeu 214
DB 611 CTGCGCGATTCAGGAGATGTGGACGAGTCTTTCGCGCTTCACGGTTCGGTTTAACTT 670
QY 215 ThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAsp 234
DB 671 GGTGATTATATCCCTTGGCTAGATTGGCTGGACCTCGAGGGGTACGTTCTAGGATGAG 730
QY 235 AspIleLeuAsnLysPheAspProValValGluArgValIle-----LysLysArg 251
DB 731 AGAATGAAGCGAGGTTTGGTCGATTCCTGGAACAGAGTCTTGAGCGTGCACACAGCGCG 790
QY 252 Arg***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal 271
DB 791 CGACTA-----CGCGAGGAGGAACTTGTGGCAAGAGAT----- 826
QY 272 ***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
DB 827 ATGTTGGAGCTGCTGCTGAGTGGCGGATGACACTAGTCTTTGAAGTCCAGCTCAGCAGG 886
QY 292 *****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
DB 887 GACAATGTTAAGGCTATCACAGACCTAATCATCGGAGCGGACCGATAGTAATCCAAC 946
QY 312 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331
DB 947 AGCGTGAAGTGGCTGCTCGGAGTCTCTCAAGAACCTCTCAAGATCTTAGCATCTTACCAAGCCCATG 1006

RESULT 11
US-09-292-768-63
; Sequence 63, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
; OTHER INFORMATION: Computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase variant
US-09-292-768-63
Alignment Scores:
Pred. No.: 9.16e-74 Length: 1762
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Score: 624.50      Matches: 147
Percent Similarity: 47.99%      Conservative: 92
Best Local Similarity: 29.52%      Mismatches: 210
Query Match: 26.06%      Indels: 49
DB: 4      Gaps: 13

US-09-857-581-66 (1-521) x US-09-292-768-63 (1-1762)

Qy 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheLe 45
Db 101 TCGAATCCCAACAAACCTA-----CTCCGAGCCCT--CCGAAGTCGCGGTGATC 151
Qy 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Db 152 GGCACCTCCACTTCCTGTGGGAGGGCTTCCACGACGCTGTAGGAGCATGCCAG 211
Qy 66 LysHisGlyProLeuPheSer****PheGlySerMetProThrValValAlaSerThr 85
Db 212 AAGTACGGCGCGTGGCGACGTCAGCTGGGAGAGTGTACTCGGTGTGTCTGCTGCG 271
Qy 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 272 GCGAGGCGACGAGGAGCGAGTGAAGTCTGGAC---CCGAACCTCCCGCACCGGTTC 328
Qy 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAlaAla*****Pro*** 124
Db 329 CAGCGATCGGTCCAGGACCATGTGTACGACAAAGATGACATCTTCAGCCCTTAC 388
Qy 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
Db 389 AAGCATCACTGGCGCCACGAGGATCGGAGTCTGTCAGACAGAGTGTGTAGCCGGAAGAC 448
Qy 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 449 GTACGGTCTCGGTACATAAGACGAGGAGGATCGAGCGCTCATCCGGTGTCTGCGG 508
Qy 165 Gln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp****Asn 184
Db 509 TCGTGGGGGAGCG-----CCGTCGACGTCACGAGGAGGAGTGTCTGAAGATGTGCTGT 562
Qy 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
Db 563 GTGCTGTGTGAGGGCGGTTCGAGGAGTGTCTCAAGACACGAGGTTCTGTGGCGGAG 622
Qy 201 IleAlaArgGluValLeuLysIle***GlyGlyTyrSerLeuThrAspPhe----- 217
Db 623 TTGTTGAAGGATCGCTGGCATTCGCGTCCGGTTCGAGCTGCGCGATCTCTACCTCTCC 682
Qy 218 -----Ile***ProLeuLys***LeuLysValGlyLysTyrGluLysArg 232
Db 683 TCATGGCTCTCAACCTGCGCTAGCTTGACACATACAGGTTCGAGAGGATGCGCCCGCC 742
Qy 233 IleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg 252
Db 743 CTCGATCACATCTGTATGGTTC-----CTGGAGGAGCATAGG 781
Qy 253 ***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal*** 272
Db 782 -----GAGAAGAACGCGCGGAGTTCGAGCGGAGGAC 814
Qy 273 Leu---AspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
Db 815 ATCTCCGACGTTCTTTTCAGGATGCAGACGCGGACGACATCAAAATTCCTATCTTCC 874
Qy 292 *****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
Db 875 AATTGCATCAAGGGTTTCATTTTCGACACCTTCTCCGCGGAGCTGAACGCTCTTCGAG 934
Qy 312 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331
Db 935 ACCATCTCATGGGGGTGTCTGGAACTGATGAGAAATCCGGCGAAGATGGCCAAAGTCCAG 994
Qy 332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsn 951

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RESULT 12

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US-09-172-339-5
; Sequence 5, Application US/09172339
; Patent No. 6291745
; GENERAL INFORMATION:
; APPLICANT: Euclyaire Meyer, Terry
; APPLICANT: Valpani, Nasser
; TITLE OF INVENTION: Limonene and Other Downstream
; TITLE OF INVENTION: Metabolites of Geranyl Pyrophosphate for Insect Control in
; FILE REFERENCE: 5718-65
; CURRENT APPLICATION NUMBER: US/09/172,339
; CURRENT FILING DATE: 1998-10-14
; EARLIER APPLICATION NUMBER: 08/449,061
; EARLIER FILING DATE: 1995-05-24
; EARLIER APPLICATION NUMBER: 08/153,544
; EARLIER FILING DATE: 1993-11-16
; EARLIER APPLICATION NUMBER: 08/042,199
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Mentha spicata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Carveol Synthase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(1507)
US-09-172-339-5

Alignment Scores:
Pred. No.: 7,978-73      Length: 1762
Score: 617.50      Matches: 145
Percent Similarity: 48.58%      Conservative: 95

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Query Match:	29.35%	Mismatches:	213
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QY	26	SerLysAlaLeuArgHisLeuProAsnProSerPro**ProArgLeuProPheIle	45
DB	101	TCGAATCCCAACAACCTA-----CTCCGAGCCT--CCGAAGCTCCCGGTATC	151
QY	46	GlyHis**HisLeuLeuLysAspLysLeuHisTyrAla**IleAspLeuSerLys	65
DB	152	GGCCACCTCCACTCTCTCGGGAGGCTTCCCGACGCTGTTAGAGCATAGCCAG	211
QY	66	LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThr	85
DB	212	AACTAGGGCGGTGGCGACATGTCAGCTGGGAGAAAGTGTACTCGGTGGTCTCTCGT	271
QY	86	ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe**ThrArgPhe	105
DB	272	GGGAGGACCGCGGAGCGATGAAGGTGTGGAC---CCGAACCTTCGCGGACCGGTTC	328
QY	106	GlnThrSerAla***Arg**LeuThrTyrAsp-----*****ValAla*****Pro**	124
DB	329	GAGCGCATCGGTCCAGGACCATGTGGTACGACAAAGATGACATCATCTTCAGCCCTAC	388
QY	125	GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThr	144
DB	389	ACGATCATCGGCGCATGCGGAGATCGGTGACAGAGCTGCTGAGCCCGGAGAAC	448
QY	145	ValAsn**LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg**MetAla	164
DB	449	GTCAGGTCTTCGGGTACATAGGACGAGGAGATCGAGCGCTCATCTCGGCTCTCGG	508
QY	165	Gln***AlaGluAla***LysProLeuAsp***hrGluGluLeuLeuLysTrp**Asn	184
DB	509	TGCTCGGGGGAGCG-----CCGTCACCTGACGGAGGAGGTGTCGAAGATGCTCGT	562
QY	185	SerThr**SerMetMet**LeuGly-----GluAlaGluGluIleArgAsp	200
DB	563	GTGCTGTGTGCGGCGCGCTTCGGAGTGTGCTCAAGGACCGGGTTCGTTGGCGGAG	622
QY	201	IleAlaArgGluValLeuLysIle**GlyGluTyrSerLeuThrAspPheIle**Pro	220
DB	623	TTGGTGAAGGATCGCTGCGATGCGGCGGTTTACGCTGGGGAT---CTCATCCT	679
QY	221	-----LeuLys**LeuLysValGlyLysTyrGluLysArgIleAspAspIle	236
DB	680	TCTCATGCTCTCAACCTGCTTACCTTGACACATAC-----AGTTGACAGAGATG	733
QY	237	LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg**IleValArg	256
DB	734	CGCGCGCGCTCGATCACATCTTGTGCTGAGGAGCATAGG-----	781
QY	257	ArgArg**AsnGlyGlu*****GluGlyGlu**SerGlyVal**Leu---AspThr	275
DB	782	-----GAGAGAGAGCGCGGACCTTGGAGCGGAGGACATCTCGACGTT	826
QY	276	LeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys*****IleLys	295
DB	827	CTTTTCAGGATGACGCGGCGGACGACAGCAAAATTCCTACTTCCAAATTCATCAAG	886
QY	296	GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp	315
DB	887	GGTTTCATTTCGACACCTCTTCGCGGGAGCTGAACGCTCTTCGACGACCATCTCATG	946
QY	316	AlaLeuAlaGluLeuIleAsnAsnPro**ValLeu*****AlaArgGluGlu**Tyr	335
DB	947	GCCTTCGGAATGATGAGATCCGCGAAGATGCGCAAGGTGCGCGCGGAGGTAGA	1006
QY	336	SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle	355
DB	1007	GAGCGCCTCAAGGAAAGACATCTGGATTGACGAGGTGCGAAGAGCTAAAATAGCTG	1066


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:   N A M E :   P e r r y ,   L a w r e n c e   S .
:   R E G I S T R A T I O N   N U M B E R :   31865
:   T E L E C O M M U N I C A T I O N   I N F O R M A T I O N :
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:   T E L E F A X :   212-218-2200
:   I N F O R M A T I O N   F O R   S E Q   I D   N O :   63   :
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:   S T R A N D E D N E S S :   d o u b l e
:   T O P O L O G Y :   l i n e a r
:   M O L E C U L E   T Y P E :   c D N A   t o   m R N A
:   O R I G I N A L   S O U R C E :
:   O R G A N I S M :   E u s t o m a   r u s s e l l i a n u m
:   F E A T U R E :
:   N A M E / K E Y :   C D S
:   L O C A T I O N :   92   t o   1621
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:   I D :   08-606-505B-63

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Indels:	69
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US-09-857-581-66 (1-521) x US-08-606-505B-63 (1-2174)

[illegible]

Qy	193	----	GlyGluAlaGluGluLeuArgAspIleAlaArg	203
Dd	671	AGCAACGAGT	TTTCGGGTCTCAAGGATCAAAATCAAGATTCAAGATATGGTGTT	730
Qy	204	GluValLeuLysIle***GlyGluTyrserLeuThrAspPheIle***ProLeuLys***	223	
Dd	731	CAGTTGACTGTTCTCGCTATTTCAACATAGTAGATTATTCCTCCCTCGATTGCATG	790	
Qy	224	LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVal	243	
Dd	791	ATGGATTTCAGGGGATTCAGGCGGAATAAACAAGTTCATAGAAGTTTGATGCTTG	850	
Qy	244	ValCuuGValIleLysLysArgArg**IleValArgArg---	258	
Dd	851	TTGACTCGGTTGCTGGAAGACACATGCTCGCTCATCGGTAAAGCACGCCCTGAT	910	
Qy	259	-----***AsnGlyGlu****GluGlyGlu***SerGlyVal***	272	
Dd	911	TTCTCTGATTTTCGTTGCAATGCGCAATCTGAAGCGAA-----	935	
Qy	273	LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys***	292	
Dd	956	-----AGGCTTCAGACAGTC	970	
Qy	293	**IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****	312	
Dd	971	AATATCAAGGCTCTTTATTGAACATGTTTACCCTGTTACGGATACATCTTCAAAGCGTC	1030	
Qy	313	ThrGluTrpAlaLeuAlaGluIleAsnAspPro**ValLeuLys****AlaArgGlu	332	
Dd	1031	ATAGATGGCGCTGCCGAGTTCCTTAAGAAATCCAATCATCTAGACAGAGCCCAAGAA	1090	
Qy	333	Glu***TyrservalValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeu	352	
Dd	1091	GAATGACGCGTGTGATGCGCGCAGCGCGGTTCTTTCAGGACAGACATATCAAAAGTTG	1150	
Qy	353	ProTyrlleArgAlaIleValLysGluThrPheArgMethIserProLeuProVal---	371	
Dd	1151	CCATATCTCCAAAGCATCTCAAGAAGSCTTTCAGAAGCATCTCTCCAGCGCTTTAAAT	1210	
Qy	372	ValtyrArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAla	391	
Dd	1211	CTCCCCAGAAATCGCTCGCAAGCATGTGAAGTAAATGACACTACATACCAAAGGCGACT	1270	
Qy	392	Leu****PheAsnValTrpGlnValGly***Asp***LysTyrrtrPaspArgProSer	411	
Dd	1271	AGGCTCAGCGTTAACATATGGGTATTGGAGAGATCCATCTCTGTGGGAAAATCCAAAT	1330	
Qy	412	Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAsp	431	
Dd	1331	GAATTTAAACCCCTGATAGGTTTTTGGACGA-----AAGATGCCAAGATCGAT	1378	
Qy	432	LeuArggly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly	451	
Dd	1379	CCACGAGGAATAGATTTTGACTGATCCCATTGGAGCTGGAGAGAGAATTTCCGCTGGA	1438	
Qy	452	Val***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAsp	471	
Dd	1439	ACAAGATTGGGAATACTCTFAGTGGAGATATATTGGGAACCTTTGGTGCATCTCTTTGTT	1498	
Qy	472	LeuClnValLeuGlyProGlnGlnIleLeuLysGly***AspAlaLysValSerMet	491	
Dd	1499	TGGGAATG-----CCATCTCTCTGTGATT-----GACCTTACATG	1534	
Qy	492	GluGluArgAlaGlyLeuThrValProArgAlahisSerLeuValCysValProLeuAla	511	
Dd	1535	GATGAGCTTTTGGGCTTGCTCTGCAGAAAGCA-----GTGCGCTCTGCT	1579	

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Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 1, 2003, 01:40:43 ; Search time 237 seconds

(without alignments)
2964.128 Million cell updates/sec

Title: US-09-857-581-66.

Perfect score: 2396

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.5	25.7	1554	9	US-09-938-842A-1009 Sequence 1009, Ap
2	593.5	24.8	1539	9	US-09-938-842A-199 Sequence 199, App
3	582.5	24.3	2174	10	US-09-814-786-63 Sequence 63, Appl
4	575.5	24.0	1927	10	US-09-814-786-64 Sequence 64, Appl

5	574.5	24.0	1824	10	US-09-814-786-1	Sequence 1, Appli
6	574	24.0	1575	9	US-09-938-842A-1997	Sequence 1997, Ap
7	568.5	23.7	1764	10	US-09-947-0027-3	Sequence 3, Appli
8	568.5	23.7	1764	12	US-10-091-009-3	Sequence 3, Appli
9	563.5	23.5	1563	9	US-09-938-842A-1506	Sequence 1506, Ap
10	563	23.5	1545	9	US-10-142-231-55	Sequence 55, Appl
11	563	23.5	1933	9	US-10-067-534-1	Sequence 1, Appli
12	559	23.3	1509	9	US-09-938-842A-2124	Sequence 2124, Ap
13	556	23.2	1397	10	US-09-878-574-72	Sequence 72, Appl
14	553	23.1	1431	9	US-09-938-842A-2690	Sequence 2690, Ap
15	552	23.0	1539	9	US-10-142-231-53	Sequence 53, Appl
16	546.5	22.8	1883	10	US-09-796-256A-3	Sequence 3, Appli
17	545.5	22.8	1557	9	US-09-938-842A-2669	Sequence 2669, Ap
18	531.5	22.2	1479	9	US-09-938-842A-2172	Sequence 2172, Ap
19	529	22.1	1488	9	US-09-938-842A-1189	Sequence 1189, Ap
20	527	22.0	1929	9	US-09-899-643-1	Sequence 1, Appli
21	523.5	21.8	1503	9	US-09-938-842A-61	Sequence 61, Appl
22	520.5	21.7	1506	9	US-09-938-842A-2354	Sequence 2354, Ap
23	516.5	21.6	1515	9	US-09-938-842A-1301	Sequence 1301, Ap
24	511.5	21.3	1494	9	US-09-938-842A-2278	Sequence 2278, Ap
25	510	21.3	1512	9	US-09-938-842A-638	Sequence 638, App
26	505.5	21.1	1515	9	US-09-938-842A-655	Sequence 655, App
27	503	21.0	1473	9	US-09-938-842A-2477	Sequence 2477, Ap
28	497.5	20.8	1634	10	US-09-887-576-614	Sequence 614, App
29	496	20.7	1548	9	US-09-938-842A-1541	Sequence 1541, Ap
30	494.5	20.6	1488	9	US-09-938-842A-1188	Sequence 1188, Ap
31	489	20.4	1509	9	US-09-938-842A-1499	Sequence 1499, Ap
32	488.5	20.4	1503	9	US-09-938-842A-1473	Sequence 1473, Ap
33	487	20.3	1557	9	US-09-938-842A-1959	Sequence 1959, Ap
34	479	20.0	1494	9	US-09-938-842A-1382	Sequence 1382, Ap
35	475	19.8	1527	10	US-09-931-267-1	Sequence 1, Appli
36	475	19.8	1549	10	US-09-931-267-3	Sequence 3, Appli
37	473.5	19.8	1473	9	US-09-938-842A-814	Sequence 814, App
38	473	19.7	1527	10	US-09-931-267-2	Sequence 2, Appli
39	473	19.7	1708	10	US-09-796-256A-1	Sequence 1, Appli
40	472.5	19.7	1509	9	US-09-938-842A-835	Sequence 835, App
41	444	18.5	1990	10	US-09-349-385-9	Sequence 9, Appli
42	433	18.1	1473	9	US-09-938-842A-1300	Sequence 1300, Ap
43	429.5	17.9	1902	10	US-09-349-385-2	Sequence 2, Appli
44	428	17.9	806	10	US-09-770-445-795	Sequence 795, App
45	421.5	17.6	876	10	US-09-770-445-543	Sequence 543, App

ALIGNMENTS

RESULT 1
US-09-938-842A-1009
: Sequence 1009, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: FILE REFERENCE: SCRI1300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: PRIOR FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1009
: LENGTH: 1554
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1009
Alignment Scores:

TITLE OF INVENTION: NOVEL PLANT GENES
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112-3801

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette - 3.50 inch, 720 kb storage.
 COMPUTER: IBM PS/V
 OPERATING SYSTEM: MS-DOS Ver3.30
 SOFTWARE: PATENT AID Ver1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/814,786
 FILING DATE: 23-Mar-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE: 14-Jul-2000
 APPLICATION NUMBER: JP44963/92
 FILING DATE: 02-MAR-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Perry, Lawrence S.
 REGISTRATION NUMBER: 31865

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-218-2100
 TELEFAX: 212-218-2200

INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:

LENGTH: 1927 base pairs
 TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
 ORIGINAL SOURCE:

ORGANISM: Campanula medium

FEATURE:
 NAME/KEY: CDS
 LOCATION: 180 to 1748
 IDENTIFICATION METHOD: by experiment
 SEQUENCE DESCRIPTION: SEQ ID NO: 64
 US-09-814-786-64

Alignment Scores:
 Pred. No.: 2,72e-74 Length: 1927
 Score: 575.50 Matches: 141
 Percent Similarity: 48.02% Conservative: 101
 Best Local Similarity: 27.98% Mismatches: 212
 Query Match: 24.02% Indels: 50
 DB: 10 Gaps: 11

US-09-857-581-66 (1-521) x US-09-814-786-64 (1-1927)

Qy 33 ProAsnProProSerPro***ProArgLeuProPheLeuGlyHis***HisLeuLeuLy 52
 Db 284 CCACACCTCCCTCCCGGCCCAACCGGATGCGCGATCATCGGCGCCCTCCACCTTA-- 341
 Qy 52 sAspLysLeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSe 72
 Db 342 -GGCACCATGCCACATGTTTCCTTAGCCGACATGCGCGTTAAATACGGTCTATAATGTA 400
 Qy 72 r*****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuph 92
 Db 401 CTTAAACTTGGTTCAAAGGGGACCGCTGCGCCCTCAATCAAAAGCGCGCCGCGCTT 460
 Qy 92 eLeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg** 112
 Db 461 CTTGAACCCCATGATGCC---ARTTTTCTAACCGCTCGGATGTATGGGGCCCTACCTA 517
 Qy 112 *LeuThrTyrAsp***-----ValAla*****Pro***GlyProTyrTrp***PheVa 131
 Db 518 CCTCGGTATAATGCACAGACATGGTTTTTTCAGATAATGCGCCCAAAATGGAAGCTTTT 577

Qy 131 lAtcLysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLe 151
 Db 578 CGGAAGCTATGTAGCTTGACATGTTAGGCCCAAGGCACTCGAGGATGGGCTCATGT 637
 Qy 151 uArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***Ly 171
 Db 638 CAAAGTTTCAGAGGTCGTCATATGCTCAAAGAAATGTACGAGCAATCGAGTAAGTCAGT 697
 Qy 171 sProLeuAsp---***ThrGluGluLeuLeuLysTrp***AsnSerThr----- 186
 Db 698 GCCAGTCCAGTGTGTGTCGACAGATGTTAACTTATGCCATGCTAATATGATGTGACG 757
 Qy 187 -----***SerMetMet** 191
 Db 758 AATCATACTCAGCGCGCCCTTTTGTATACGAGCAAAATTAGACTCGTCTCTCTCTGC 817
 Qy 191 *LeuGlyGluAlaGluIleArgAspIleAlaArgGluValLeuLysIle***GlyG 211
 Db 818 TTCTGCTTCTGTTAGTAGAATTCCAATATATGGTTATGGAGCTCATGAGGATGCGAGGTT 877
 Qy 211 uTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLy 231
 Db 878 GTTCATATTGGTGATTTTCATACCATATATTGCGATGATGATTCGACGGCATTCACG 937
 Qy 231 sArgIleAspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysAr 251
 Db 938 TGATATGAAGGTTATACAGAAAGATTGATGCTTGTGTGAACAAATATGATCAAGGAACA 997
 Qy 251 gArg***IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVa 271
 Db 998 TACAGATCCGCTCATGCTCGCAAGATAATCTGTAT----- 1034
 Qy 271 l***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLy 291
 Db 1035 -TTTCTTGATATTCTTAGCGGCTACCCAAAGAAACACGCGGAGGATTCAGCTTAATCT 1093
 Qy 291 s*****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla** 311
 Db 1094 TGTAATGTTAAGGCACCTCTTTGGATTATTACCGCGGGACGAGGATACATCACTACAG 1153
 Qy 311 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaAr 331
 Db 1154 TGTGATCGAATGGGCACTACCGCAATGTTGAACCATCGACAGATCTAAACCGGGCCCA 1213
 Qy 331 gGluGlu**TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAs 351
 Db 1214 CGAAGAAATGGCAACTCATTCGAGAAACAGAGAACTAGAACATCTGACATACCAAA 1273
 Qy 351 nLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProVa 371
 Db 1274 CTTGCCATATTTCCAGGCCATATGCAAGAAACATTCGGAACACACCCCTCCACGCCCTT 1333
 Qy 371 l---valLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGluG 390
 Db 1334 AAACCTCCCAAGATCTCAACAGACGATCTGAAGTGGACGGGATTCACATACCAAAA 1393
 Qy 390 yAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArg 410
 Db 1394 CACTAGACTAATAGTGAACATATGGCAATAGGAGGAGCCCTAAAGTGTGGGAAATCC 1453
 Qy 410 oSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****Le 430
 Db 1454 ATTAGATTTTACTCCGAGCGCTTCTTGTAGTGAA-----AAACACCGCAAAAT 1501
 Qy 430 uAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysPr 450
 Db 1502 TGATCCCGGAGGTAATCATTTTGAGTTAATCCCATTTTGGGGCTGGGACGAGGATATGTC 1561
 Qy 450 oGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPh 470
 Db 1562 AGGGCTAGAAATGGGAGCGGCTCGGTGCGAGTACATATTAGGTACATTTGTTGTCACCT 1621

QY 470 eAspLeuGlnValLeuGlyProGlnGlyGlnLeuLeuLysGly***AspAlaLysValse 490
Db 1622 TGATTGAAATG-----CCTGAGGAGTTGTG-----GAAGTTAA 1657
QY 490 rMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProle 510
Db 1658 TATGGAAGAGAGTTTGGGATGCATGCAAAAAA-----GTGCTCT 1702
QY 510 uAlaArgile 513
Db 1703 TTCTGCTATT 1712

RESULT 5

US-09-814-786-1
Sequence 1, Application US/09814786
Patent No. US20020100072A1
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Yasuhiro
KIKUCHI, Yasuhiro
SHIMADA, Yukihisa
OHBAIASHI, Masaya
SHIMADA, Ritsuko
OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/4
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,786
FILING DATE: 23-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-Jul-2000
APPLICATION NUMBER: JP44963/92
FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Perry, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1824 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Petunia hybrida
STRAIN: Falcon Blue
FEATURE:
NAME/KEY: CDS
LOCATION: 116 to 1633
IDENTIFICATION METHOD: by experiment
SEQUENCE DESCRIPTION: SEQ ID NO: 1

US-09-814-786-1

Alignment Scores:
Pred. No.: 3,51e-74 Length: 1824
Score: 574.50 Matches: 151
Percent Similarity: 45.51% Conservative: 92
Best Local Similarity: 28.28% Mismatches: 224

Query Match: 23.98% Indels: 67
Db: 10 Gaps: 13
US-09-857-581-66 (1-521) x US-09-814-786-1 (1-1824)
QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***Val---LeuAlaLeuPhe***HisLeuArg 19
Db 116 ATGATGCTACTACTAGCTGTGTCAGCACTTCAATCTTCTAATAGCACATAATC 175
QY 20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro*** 39
Db 176 ATTTCACTCTTATTTCAAAACACTACCGCGGCTCTACCG-----CCGGG 223
QY 40 ProArg---LeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyr 58
Db 224 CCAAGAGGGTGGCGGCTGATCGGAGCACCTTCCACTTTTA---GGAGCCATGCCACATGT 280
QY 59 Ala***IleAspLeuSerLysLysHisGlyProLeuPheSer***PheGlySerMet 78
Db 281 TCCTTAGCTAAATGGCAAAAAATATGGAGCAATCATGTATCTCAAGTTGGAACATGT 340
QY 79 ProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln***GluAla 98
Db 341 GGCATGGCAGTTGCTTCTACCCCTGATGCTGCTAAAGCATCTTGAAACACATGAT--- 397
QY 99 ThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*** 117
Db 398 ATCAACTTCTCCAATCGTCCACTTAATGCAGGTGCCACTCCTACTAGCTTATAATGCTCAA 457
QY 118 **ValAla****Pro***GlyProTyrTyr***PheValArgLysLeuIleMetAsn 137
Db 458 GACATGGTTTTTGCACATTATGGACCCAGCATGGAGTTGCTAGGAATTAAGCAACTTG 517
QY 138 AspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArg 157
Db 518 CATATGCTAGGGGAAAGCCCTTAGAGATTGGCAATGTGTGCTGCAATAGCTAGG 577
QY 158 Lys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlu 177
Db 578 CACATGCTAAATCAATGCTCGATATGATCGAGAGGGCCAGAGGGTGTGTGGCGGAG 637
QY 178 GluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
Db 638 ATGTTGACATTTGCCATGGCCAAATATGATCGGACAGTGTAGTGAAGCAAAAGATATT 697
QY 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle 208
Db 698 GTAGATAAGGTGTTGAGGTAAATTAAGGACATGTTGTAGAGTTAATGACAATA 757
QY 209 **GlyGlyTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLys 228
Db 758 GCAGGTATTTCAACATTTGTTGATTTTATTCTCTTTTGTAGCTTGGATGATTTACAAGG 817
QY 229 TyrGlyLysArgIleAspAspIleLeuAsnLysPheAspProValValGluArgValIle 248
Db 818 ATAGAAAACGATGAACCGTTTACATAAGAGTTGATGCTTTATTGACAAAGATGTTT 877
QY 249 LysLysArgArg***IleValArgArg----- 258
Db 878 GATCAACACAAAGCAACTACCTATGACGTAAAGGGAAACACAGATTTCTTGTATGTTGT 937
QY 259 ----**AsnGlyGlu****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeu 277
Db 938 ATGGAATGGGCAATTTCTGAAGGAGAA----- 967
QY 278 GluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeu 297
Db 968 -----AGACTCAGTACCAACCAACATCAAGACATT 997
QY 298 ValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeu 317
Db 998 TTGCTGAATTTGTCACAGCTGTGACGACACTTCTTCTAGTGAATAGATAATGGCACATT 1057

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QY 318 AlaGluLeuIleAsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerVal 337
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Db 1058 GCAGAAATGATGAGAGACCTGCCATTTTGAAGAGCAGACAGAGATGATCAGTC 1117

QY 338 ValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAla 357
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Db 1118 ATTGAAGAAATAGCGCTTTACTCGAATCCGATATCCCAATCTCCCTTACTCCGAGCA 1177

QY 358 IleValLysGluThrPheArgMetHisProLeuProVal---ValLysArgLysCys 376
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1178 ATTGCCAAGAAACATTTTCGAACACCCCTCTACACCATTAATCTCTCTAGATCTCG 1237

QY 377 ***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsn 396
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1238 AACGAACCATGATAGTCGATGGTTATTACATACCAAAACACATAGGCTTAGTGTAAAC 1297

QY 397 ValTyrGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGlu 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1298 ATATGGCAANTGGAGAGATCCCAAGTTTGGGAAATCCACTAGATTTAATCCCGAA 1357

QY 417 ArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***His 436
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1358 AGATTCTTG-----AGTGAAGAAACCTCCAAGATTGATCTCGAGGGAACGAT 1405

QY 437 PheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThr 456
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1406 TTGTAATTCATACCATTTGGTGCTGCGAGAGAAATTTGTGAGGAACAGAAATGGGAAT 1455

QY 457 SerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGly 476
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1466 GTAATGGTGAATATATATAGGAATTTGGTTCATTTCATTGTTGGA---1516

QY 477 ProGlnGlyGlnIleLeuGlyGly***AspAlaLysValSerMetGluGluArgAlaGly 496
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1517 -----TTACCAAGTGAAGATTATTGAGTTGAATATGGAAGAGCTTTTGGC 1561

QY 497 LeuThrValProArgAlaHisSerLeuValCysValProLeu 510
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Db 1562 TTAGCTTTTCAGAAAGCT-----GTCCCTCTT 1588
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RESULT 6

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US-09-938-842A-1997
; Sequence 1997, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1997
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1997

Alignment Scores:
Pred. No.: 3,328-74 Length: 1575
Score: 574.00 Matches: 149
Percent Similarity: 47.41% Conservative: 89
Best Local Similarity: 29.68% Mismatches: 222
Query Match: 23.96% Indels: 42
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Db 1111 CTTTACCTCAAGCGGTATGAAGAGACTCTTAGGCTTCACCTACGCTTCTCTCTT 1170
QY 372 VALLYSARGLYCYS**GluGluCys**IleAsnGly**Val**ProGluGlyAla 391
Db 1171 GTTCTCAGCAAAACAGCGAACCTCGGCGGTGGGATACACACTGTCCCTAAAGACTCC 1230
QY 392 Leu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSer 411
Db 1231 AAGATTTCATCAACGTTTGGCGGATTCATAGAGATCTCAGAAATGGATGACCAAC 1290
QY 412 Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAsp 431
Db 1291 GAGTTCAAACCTCAGAGGTTTGGAGAAAT-----TCGCTTGAT 1329
QY 432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly 451
Db 1330 TTCAATGGAGGATTTTAAGTACTTGCTTTTGGGTAGGAGAGATTTGCGCGG 1389
QY 452 Val***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAsp 471
Db 1390 ATTAACATGCTCAGAGACTTGTCTGTTCACATTTGCTTCTTCACTTCTTCACTTCTTGCAT 1449
QY 472 LeuGluValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMet 491
Db 1450 TGGAAA-----GCACCTCAGACAG-----AAGTTTGAGGTT 1482
QY 492 GluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAla 511
Db 1483 GAAGAGAAGTTGGTCTTCTTCTTAAGTTGAAGTCTCCACTTGTGCTATTCCTTCCA 1542
QY 512 ArgIle 513
Db 1543 AGGTTG 1548

RESULT 7

US-09-947-027-3
; Sequence 3, Application US/09947027
; Patent No. US20020124281A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laiqeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITION
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: CAID5H
US-09-947-027-3

Alignment Scores:

Pred. No.: 2,57e-73 Length: 1764
Score: 568.50 Matches: 146
Percent Similarity: 46.14% Conservative: 87
Best Local Similarity: 28.91% Mismatches: 231
Query Match: 23.73% Indels: 41
DB: 10 Gaps: 13

US-09-857-581-66 (1-521) x US-09-947-027-3 (1-1764)

QY 26 SerLysAlaLeuArgHisLeuProAsnProSerPro***ProArgLeuProPheIle 45
Db 155 TCTCGCCTTGGCGGAAGATTGGCATATCCACCAGGCGCT---AAAGGGTTGCCACTTGA 211

QY 46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSerLys 65
Db 212 GGTAGCATGCACATGATG---GACCAATAACACACCGGTAGGTAGTAACATAGTAA 268
QY 66 LysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaLaserThr 85
Db 269 CAATATGGTGGCTCTTTTCATATGCGCATGGGTACTTCATATGTCATGTCATGTTTCATCT 328
QY 86 ProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
Db 329 CCTGAATAGTCCCAAGTCTCGCAGTCCAGGAC---AACATTTTCTCCACAGACCA 385
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp---*****ValAla*****Pro*** 124
Db 386 GCCAATAGTCCATAAAGTACTTAACTATGATCGTCAGATATGGCTTTGCCACTAC 445
QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThr 144
Db 446 GGTCTTTTCTGGCAGACAGATCGTAACTCTGCTAGCTGCTGAGCTTTTACCCGAAA--- 502
QY 145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
Db 503 -----AGCGCTGAATCATGGAGTCTGTGACATGAGGTGGACTCAATGCIT 550
QY 165 Gln***AlaGluAla-----LysProLeuAsp***ThrGluGluLeuLysTrp 182
Db 551 AAGACAGTTGAAGCAATATAGCAGACCTGTGAATCTTGGGAATTTGATTTTACGTTG 610
QY 183 ***AsnSerThr***SerMetMet***LeuGluGluAlaGluGluIleArgAsp----- 200
Db 611 ACCATGAACATCACTACAGACAGCTTTCGGGCTGCTGAGCATGAGGTGGACTGAGTTC 670
QY 201 -----IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle 218
Db 671 ATCAAGATTTTGCAGGAGTTCTCTAAGCTTTTGGACATTCACATGCTGATTTTCAT 730
QY 219 ***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsn 238
Db 731 CCCTGGCTGGCTGGATTGACCCCAAGGCTACGCTAGCTTGTCAAGGTCGCAAG 790
QY 239 LysPheAspProValValGluArgValIleLysLysArg***IleValArgArgArg 258
Db 791 GCTCTTGATAGATTCATCGACTCTATCATCGATCATCAT-----ATCCAGAAAGAAAA 844
QY 259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlu 278
Db 845 CAGATAAGTTCTCTGAAGATGCTGAAACCGCATATGCTC-----GATGACATGCTAGCC 898
QY 279 Phe-----AlaGluAspGluThr***GluIleLys 288
Db 899 TTTTATGCTGAAGAAGCAAGAAAGTAGATGAATCAGATGATTTACAAAAGCCATCAGC 958
QY 289 IleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly***AspSer 308
Db 959 CTTACTAAAGACAACATCAAAAGCCATATCATCGATGCTGATGTTGGTGGCAGAGACG 1018
QY 309 ThrAla*****ThrGluTrpAlaLeuAlaGluIleAsnAsnPro***ValLeu*** 328
Db 1019 GTGGCGTCGCCAATAGACTGGTTCATGCGGAGCTATGAGACTCCAGAGGATCAAAA 1078
QY 329 ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
Db 1079 AGAGTCCAGCAAGAGCTCGCAGAGGTGGTGGTTAGAGCGCGCGCTGGAGGAAGTAT 1138
QY 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
Db 1139 ATTGACAAACTTACGTTCTTGAATGCGCCCTCAAAACAACTTAAAGATGACCCACCA 1198
QY 369 LeuProValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
Db 1199 ATCCACATCTCTTACATGAACACTCTCAGGATGCTGAGGTGCTGTTTATTTTCATCCA 1258

Qy	389	GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp	408
Db	1259	AACCAACAAGGGTGATGATCAAATGTCTATTCATTGGGAGACAGAATTCATGGGA	1318
Qy	409	ArgProSerGlu***ArgProGluAArgPheLeuGluThr***AlaGluGlyGluAla***	428
Db	1319	GATCCTCATGCTTTTAAGCCCTTCAGGTTTTGAACAGGGGTGCCT-----	1366
Qy	429	***LeuAspLeuArgGly***HisPheGlnLeuLeuLeuProPheGlySerGlyArq***Met	448
Db	1367	-----GATTTAAAGGGAATCACTTTGACTTTATTCCTTCGGGTCTGTCGGAGGTCT	1420
Qy	449	CysProGlyVal***LeuAlaThrSerGly**AlaThrLeuLeuAlaSerLeuLeuGln	468
Db	1421	TGCCCGGTATGCAGCTTGGGTATAACACTTGATTTGGCTGTGCTACTTGCTTCAT	1480
Qy	469	CysPheAspLeuGlnValLeuGlyProGlnGlyClnIleLeuLysGly***AspAlaLys	488
Db	1481	TGTTTACATGGGAATG-----CCUGATGGCATG-----AAACCGAGTGAA	1522
Qy	489	ValserMetGluGlnArgAlaGlyLeuThrValProArgAlaHisSerLeuValcysVal	508
Db	1523	CTTCACATGACTGNATATGTTTGGACATCACCGGCCAACAGCACTGCATCGTTCGGGT	1582
Qy	509	ProLeuAlaArgIle	513
Db	1583	CCGAGCAAGCGTGTG	1597

RESULT 8

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US-10-091-009-3
; Sequence 3, Application US/10091009
; Patent No. US20020138870A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Vincent Lee C.
; APPLICANT: Li, Laigeng
; TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
; TITLE OF INVENTION: COMPOSITION, AND
; TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
; FILE REFERENCE: 066040-9718
; CURRENT APPLICATION NUMBER: US/10/091,009
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: 09/947,027
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 60/230,086
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: aspen populus tremuloides
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Calcd5H
US-10-091-009-3

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US-09-857-581-66 (1-521) x US-10-091-009-3 (1-1764)

QY 26 SerLysAlaLeuArgHisLeuProGAsnProProSerPro***ProArgLeuProPheLe 45
Db 155 TCTCGCCTTCGCGAAGATTCCTATCCACAGGCCT--AAAGGGTGGCCACTGTGA 211
QY 46 GlyHis***HisLeuLeuAspLysLeuHisLeuHisTyAla***IleAspLeuSerLys 65
Db 212 GTAGCATGCACATGATG--GACCAATAACTCACCGTGGGTAGCTAAACTAGCTAAG 268

QY 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
 Db 1319 GATCTGATGCTTTTAAAGCCTTCAAGTTTGTAAACAGAGGTCCT----- 1366
 QY 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
 Db 1367 -----GATTTTAAAGGAATCAGCTTTGAGTTTATTCCTTTTCGGGCTCTGGCGAGGTCT 1420
 QY 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
 Db 1421 TCCTCCGGTATGACCTTGGGTATACACACTTGATTTGGCTGTTCCTCACTTGCCTCAT 1480
 QY 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
 Db 1481 TCTTTTACATGGGAATG-----CCTGATGCGATG-----AAACCGAGTGAA 1522
 QY 489 ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
 Db 1523 CTTCGATGACGATATGTTGGACTCACCGCGCCCAAGCAACTCGACTCGTTGCCGTT 1582
 QY 509 ProLeuAlaArgIle 513
 Db 1583 CCGAGCAAGCGGTG 1597
 RESULT 9
 US-09-938-842A-1506
 ; Sequence 1506, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPT300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1506
 ; LENGTH: 1563
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1506
 Alignment Scores:
 Pred. No.: 1,17e-72 Length: 1563
 Score: 563.50 Matches: 146
 Percent Similarity: 45.45% Conservative: 94
 Best Local Similarity: 27.65% Mismatches: 241
 Query Match: 23.52% Indels: 47
 DB: 9 Gaps: 14
 US-09-857-581-66 (1-521) x US-09-938-842A-1506 (1-1563)
 QY 3 LeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro 22
 Db 55 CTTCGATCGTGTCTCTCTTTTCACTTCATCAGCTTCATCACACGGCGGGAAGGCT 114
 QY 23 ***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeu 42
 Db 115 -----CCATATCTCCCGTCCACGA---GGTTGG 141
 QY 43 PropHeIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisThrAla***IleAsp 62
 Db 142 CCATCATAGGCAACATG---TTAATGATGGACCAACTCACCCACCGCTGTTAGCCAA 198

QY 63 LeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal 82
 Db 199 TTAGCTAAAGATATGGCGATTTGCCATCTCCCGATGGATTCCTCCATATGACGCT 258
 QY 83 AlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe*** 102
 Db 259 GTCTCATACCGAGGTGGCTCGACAAAGTCTTCAAGTCCAAAGACAGCCT---TTCTCG 315
 QY 103 ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp---A*****ValAla*** 121
 Db 316 AACGGGCTCCACTATAGCTATAGCTATCTAGCTTAGCAGCGGACGACATGGCTTTC 375
 QY 122 ***Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsn 141
 Db 376 GCTCACTACGACCGCTTTTGGACAGAGATGAGAAAAGTGTGTCTCAAGGTGTTTACG 435
 QY 142 AlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg 161
 Db 436 CGTAAAGAGCTGAGTCATGGGCTTCAGTTCGT---GATGAGTGGACAAATGGTCCGG 492
 QY 162 ***MetaAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLys 181
 Db 493 TCGTCTCT-----TGTAACGTTGGTAAAGCTATAAAGCTCGGGGAGCAAAATTTTGA 546
 QY 182 Trp***AsnSerThr***SerMetMet***LeuGlyGluAla-----Glu 196
 Db 547 CTGACCCCGCAACATACTTACCGGGGAGCGTTTGGGTACGCTCGGAGGAGGACAGAC 606
 QY 197 GluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAsp 216
 Db 607 GAGTTCATAAGAACTCTTACAAGAGTTCTCTAAGCTTTTGGAGCTTCAACAGTACGGAT 666
 QY 217 PheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIle 236
 Db 667 TTATACCATATTTCGGTGGTTCGATCCCGAAGGATTAACAGCGGCTCTGTGAGGCG 726
 QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
 Db 727 CGTAATGATCTAGACGGATTTATTGAGATATTATCGATGAACAT-----ATGAAGAAG 780
 QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
 Db 781 AAGGAGAAATCAAAACGCTGTGGATGATGGGATGTTGTGATACCATGATGTTGATGAT 840
 QY 276 LeuLeuGluPheAlaGluAspGluThr----- 285
 Db 841 CTCTCTGCTTTTACAGTGAAGAGGCCAAATTAGTCAGTGAGACGCGGATCTTCAAAT 900
 QY 286 GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly 305
 Db 901 TCCATCAAACTTACCCGCTGACAATATCAAGCAATCATCATGACGCTTATGTTGGAGGA 960
 QY 306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnPro*** 325
 Db 961 ACGAAACGCTAGCGTCGGGATAGAGTGGCGCTTAACGAGGATTATACGACCCCGAG 1020
 QY 326 ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
 Db 1021 GATCTAAACCGGTCCCAACAGAACTCGCCGAAAGTCGTGGACTTGACAGACGAGTTGAA 1080
 QY 346 GluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMet 365
 Db 1081 GAATCCGACATCGAAGAGTTGACTTATCTCAATGACACTCAAGAAACCTTAAGATG 1140
 QY 366 HisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly*** 385
 Db 1141 CACCCACGATCCCTCTCTCCAGAAACCGGAGGAGCACTAGTATCGACGCTTC 1200
 QY 386 Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***Lys 405
 Db 1201 TTCATTCCCAAGAATCTCGTGATCATCAACCGTTTGCCTATGAGACCGGACCCCAACC 1260
 QY 406 TyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGly 425

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1261 TCITGGACTACCGGACACGTTTAGACCATCGAGGTTTITGGACCGCGGTACCG--- 1317
    ||| ||| ||||| ||||| ||||| |||||
Qy 426 GluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGly 445
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1318 -----GATTCAAGGGAGCAATTCGAGTTTATACCGTTTCGGGTCGGGT 1362
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 446 Arg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSer 465
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1363 CGTAGATCGTCCCGGTATGCACTAGGTTTATACGCGCTTGACITAGCGCGGTCTCAT 1422
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 466 LeuLeuGlnCysPheAspLeuGlnValLeuGlyProGlnGlnLeuLeuLysGly*** 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1423 ATATTACATGCTTCACGTGGAAATTA-----CCTGATGGGATG-----AAA 1464
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 486 AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeu 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1465 CCAAGTAGCTCGACATGATGTGTTTGGTCTCAGCGCTCCTRAAGCCACGCGCTT 1524
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 506 ValCysValProLeuAlaArgIle 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1525 TTCGCCGTGCCAACACCGCGCTC 1548

RESULT 10
US-10-142-231-55
; Sequence 55, Application US/10142231
; Publication No. US2003007796A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142,231
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-10-142-231-55

Alignment Scores:
Pred. No.: 1,36e-72 Length: 1545
Score: 563.00 Matches: 140
Percent Similarity: 47.99% Conservativity: 99
Best Local Similarity: 28.11% Mismatches: 211
Query Match: 23.50% Indels: 48
DB: 9 Gaps: 13

US-09-857-581-66 (1-521) x US-10-142-231-55 (1-1545)
Qy 33 ProAsnProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 112 CCACAACTCCTTCA-----TGGCCCGTTATTGGGAATCTTCATCTCCTTACA 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 53 AspLysLeu---LeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPhe 71
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 CAGAAAGTGCTATTACCGAATCTATCTTCGCTTTCGGAGAGCTATGGACCAATCATG 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 72 Ser*****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeu 91
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 220 CATCTTCAACTCGCTCCGACCAAGCTTGGTTATTCCTCTTCAGATCTTGGCGAAAGAA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 92 PheLeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 280 TGCITCACAAACAAATGAC---AAGCCCTTCGCTTCGCCACACGCTCTCTGACAGAAAG 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 112 ***LeuThrTyrAsp*****Val---Ala*****Pro***GlyProTyrTrp***Phe 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 337 CATGTAGGATATGACACAAATCTTCATGATGCTCCTTACGCTTCTACTGCGCAAC 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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131 ValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgPro 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 CTTCCGAAATTCGACGATCCAGATCCAGATCTCTCTGCAACCAAGAAATGATCTTCAGACAC 456
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 151 LeuArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGlu---Ala 169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 457 ATCCGCGTAGAAGATTTCTGCTCTCATTCGTTGCTTGTGTTGACAGTTGCCAGCGAGAG 516
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 170 **LysProLeuAsp***ThrGluGluLeuLeuLysTyr***AsnSerThr***SerMet 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 517 GACACTCCACTCAACATGAACGAGGCTCTCTGATCTCACGTTTAGTATCATCTCTCCGT 576
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 190 Met***LeuGly----- 576
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 577 ATGGTTGCCAACAAAGAAATATATCAGGACCTGTTTATCCGAGGAATAGAGAGCGGAT 636
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 197 GluIleArgAspIleAlaArgGluValLeuLysIle***GlyLysSerLeuThrAsp 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 637 CATTTTAACCATGATATAAACAGCTGTGTGTTCTTACTTGGAGCATTTGAGTTGGAGAT 696
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 217 PheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAspIle 236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 TTCCTGCCGTTTCTCAAGTGGCTTGATCTTCAAGGTTTCATAGCTGCTATGAAAAAAGTG 756
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 757 CACGAGAAAGAGATGCTTTATGAGAAATTTGGTATTGATCACCGCTAG---AAGAGA 813
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeu 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 GGGAGAGTCGATCAAAATGCACAAGAC-----TTAATTGATGTTCTC 855
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 277 LeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLysGly 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 ATCTCTGCAACAGACCAACCATGAAATTCAGTCCGATAGTAAACGACGATTTCTGAAAGCC 915
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 297 LeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAla 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 ACCGCCCTTACAATGCTGACGACGAGTACAGATACATCTCGTGACCATCAATGGGCA 975
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 317 LeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSer 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 976 TTGGCGGCTCTGATGACGACCCCTCATATTTTGGACAAAGCCGACGAGTCGACAG 1035
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 337 ValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArg 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1036 CATATCGGAGCGACCGCATTTACTAGAGAGAGAGATCTCCAGAGCTGAAATATTGAGAG 1095
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 357 AlaIleValLysGluThrPheArgMetHisProProLeuPro---ValValLysArgLys 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1096 GCAATTGTGAAGAAACGTTGAGGCTATATCCAGCGCACCTCTCTTAGTTCTCTCACGAA 1155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1156 GCATTGAGAGATTGCACTGTTGAGGGTACCATGTCCTCCGAGGACGCGCATGATTGTG 1215
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 396 AsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPro 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1216 AATGCTTGGCAATTCACAGACACCGCGCAGTGTGGAAACGCGGACCGTGTGATCTCT 1275
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1276 GAACGGTTTTTGAAGACGGGAAAGAG-----GTTGACATAAAGGCGG 1320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1321 GAGTTTGAATGATTCGTTTGGTTCAGGAGAGAATGTGTCGGGCGCATGATCTGGCA 1380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 456 ThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1381 TTGAGTGTGTTTACGTATACGCTGGGAGGCTGCTCGCAGAGTTCGAGTGTCTGT--- 1437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1438 ---CGAGGATGATGATA-----ATTGACATGACGGAGGTTG 1473
 Qy 496 GlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
 Db 1474 GGAATCAATGACCAAGCA-----GTTCCGTTGGAGACCAAT 1512

RESULT 11

US-10-067-534-1

; Sequence 1, Application US/10067534
 ; Publication No. US20020187538A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Essenberg, Margaret K.
 ; APPLICANT: Chen, Xiao-Ya
 ; APPLICANT: Luo, Ping
 ; APPLICANT: Wang, Yan-Hong
 ; TITLE OF INVENTION: cDNA Clone of (+)-Delta-Cadinene-8-Hydroxylase Gene from Cotton
 ; FILE REFERENCE: 006602-113
 ; CURRENT APPLICATION NUMBER: US/10/067,534
 ; CURRENT FILING DATE: 2002-02-07
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1933
 ; TYPE: DNA
 ; ORGANISM: Gossypium arboreum
 US-10-067-534-1

Alignment Scores:
 Pred. No.: 1,92e-72 Length: 1933
 Score: 563.00 Matches: 154
 Percent Similarity: 45.72% Conservative: 92
 Best Local Similarity: 28.62% Mismatches: 234
 Query Match: 23.50% Indels: 58
 DB: 9 Gaps: 14

US-09-857-581-66 (1-521) x US-10-067-534-1 (1-1933)

Qy 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeu----- 18
 Db 154 ATGTTGTTCCAGTACCTTGTGATTTGTTAGCCATATGGGAATTTCCATCTGGCAC 213
 Qy 19 -----ArgProThrPro***Ala***SerLysAlaLeuArgHisLeuPro 33
 Db 214 GTATGGACATAAGGAAGCCA-----AAGAAAGACATCGCCCAATTACCG 258
 Qy 34 AsnProProSerPro***ProArg---LeuProPheIleGlyHis***HisLeuLeuLys 52
 Db 259 -----CCGGGTCGCGGTGGTGGCAATAGTGGATATCTTCCATATCTTGA 306
 Qy 53 AspLysLeuLeuHisTyAla***IleAspLeuSerLysLysHisGlyProLeuPheSer 72
 Db 307 ACTGATAATCTTCACTTGGTGTTCACAGATTGGCTGACGCTTACGGTCCCATCTACAG 366
 Qy 73 *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe 92
 Db 367 CTTTGGCTAGGAACAATAATTGCGTAGTCATTAGCTCGGCACCACCTGGCCGAAGAAGTG 426
 Qy 93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
 Db 427 GTTCGTGACACGACATCACA---TTTCTGAAAGGGATCTCCCGTTTGTGCAAAAGATT 483
 Qy 113 LeuThrTyr-----Asp*****ValAla*****Pro***GlyProTyTrp***Phe 130
 Db 484 ATTACTTTGGCCTCAATGATATTGATTGTTTACAGTAGTCCAGATTGGAGATG 543
 Qy 131 ValArgLysLeuIleMetAsnAspLeuLeuAsnAlaThrValAsn***LeuArgPro 150
 Db 544 AAGAGAAAAGTCTGCTAGCTGAAATGCTTAGCCATAGTAGCATTAAGAGTTGTTATGGT 603
 Qy 151 LeuArgThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla*** 170

Db 604 CTAAGAGGAGACAGTGTCTTAAGCGGTACAAATGTGTCTCAA-----AGTCTGGC 657
 Qy 171 LysProLeuAsp***ThrGlu---GluLeuLeuLysTrp***AsnSerThr***SerMet 189
 Db 658 AAGCCAATGATTTGGTGAACGCGCATTTTAACTCAATCAATCGCATGATGACATG 717
 Qy 190 Met***LeuGlyGluAla-----GluGluIleArg 199
 Db 718 CTGTGGGTGGCAACACAGGAGAGAGCGGAAGGGCGGACGTTTGGGGCCAAATTCGA 777
 Qy 200 AspIleAlaArgGluValLeuLysIle***GlyGluTyTrpSerLeuThrAspPheIle*** 219
 Db 778 GATTCATAAACCGAATAATGCTGATCTGTAACCAACCAACGTTTCTGATATTTCGCG 837
 Qy 220 ProLeuLys***LeuLysValGlyLysTyTrpGluLysArgIleAspAspIleLeuAsnLys 239
 Db 838 GTGCTTGCAGAGTTTGACATACAGGATTGGAGAGGAATGACTAAATCGTTAAATCT 897
 Qy 240 PheAspProValValGluArgValIleLysLysArg-----Arg***IleVal 255
 Db 898 TTCGATAAGCTTTTCAACTCCATGATTGAAGAAAGAGAGAACTTTAGCAACAAATGAGC 957
 Qy 256 ArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThr 275
 Db 958 AAAGAAGATGGAACACACTGAAACAAAGAC-----TTCTTGCGAGGTT 999
 Qy 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****IleLys 295
 Db 1000 CTGTTGGACCTCAAGCAGAGAACGATACGGGAATATCGATAACATCAATCAAGTCAAG 1059
 Qy 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
 Db 1060 GCCTTCTCATGACATTTGTCGCTGGAAGTATACACATCAACCATGATGAATGG 1119
 Qy 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
 Db 1120 ACAATGGCTGACTAATTCAMATCTCGAAGCAATGAAAAGGTGAAGCAAGAATAGAC 1179
 Qy 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyIle 355
 Db 1180 GATGTTGTCGTTCCGATGGCGCGTCGATGAGACTCACTTCCTAAGTTGGCTATCTA 1239
 Qy 356 ArgAlaIleValLysGluThrPheArgMetHisProLeuProValValLysArgLys 375
 Db 1240 GATGCTGCAGTAAAGAGAGACCTTCCGATTGCCACCCACCGATGCCACTCTGTACCCGT 1299
 Qy 376 Cys-----GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu***** 394
 Db 1300 TGCCCGGGCGACTCAAGCAACGTTGGTGGCTATAGCGTACCAAGGGCCACAGGTCCTTC 1359
 Qy 395 PheAsnValTrpGlnValGly***Asp***LysTyTrpAspArgProSerGlu***Arg 414
 Db 1360 TTAACATTTGGTGTATTAGAGGGATCCACAGCTTTGGGAAATCCTTTAGAATTCAG 1419
 Qy 415 ProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly 434
 Db 1420 CCTGAGAGGTTCTTGACT-----GATCATGAGAAGCTCGCATTTATTAGA 1464
 Qy 435 ***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***Leu 454
 Db 1465 AACGATTCGCGTACATGCGGTTTGGTGTGGAGGAGAAATGTCGCCGAGTATCTCTC 1524
 Qy 455 AlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 474
 Db 1525 GTGAAAAGATGTTGATTCTCTTGGCAGCATGATCCATCTTATGATGGAACTTG 1584
 Qy 475 LeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArg 494
 Db 1585 GCGGACGCGTGAAGAAAATGACTTCAATTGGCTTA----- 1617
 Qy 495 AlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArg 512

Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 72
LENGTH: 397
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LTB3028-056-Q1-B1-F1
US-09-878-574-72

Alignment Scores:
Pred. No.: 1.81e-72 Length: 397
Score: 556.00 Matches: 112
Percent Similarity: 84.8% Conservative: 0
Best Local Similarity: 84.8% Mismatches: 20
Query Match: 23.21% Indels: 0
Gaps: 0
US-09-857-581-66 (1-521) x US-09-878-574-72 (1-397)

Qy 266 GlyGlu***SerGlyVal**LeuAspThrLeuGluPheAlaGluAspGluThr*** 285
Db 1 GGTGAGGTCACGGGGGTTTCTTGACACTTGTGTAATTCGCTGAGGATCAGACCATG 60
Qy 286 GluIleLysIleThrLys*****IleLysGlyLeuValValAsp***PheSerAlaGly 305
Db 61 GAGATCAAAATCACCAGGACCATCAAGGGCTGTGTGTGCGACTTTTCTCGCAGGA 120
Qy 306 ***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro*** 325
Db 121 ACAGACTCCACAGCGGTGCACAGAGTGGGATGGGCAATTCGACAGACTCATCAACATCCTTAAG 180
Qy 326 ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAsp 345
Db 181 GTGTTGAAAGGCTCGTGAGAGGTCTACAGTGTGTGTGGGAAAGGACAGACTTGTGGAC 240
Qy 346 GluValAspThrGluAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMet 365
Db 241 GAAGTTGACACTCAAAACCTTCCTTACATTAAGCAATCGTGAAGGACACATTCGCGATG 300
Qy 366 HisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly*** 385
Db 301 CACCGCCACTCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGTGAGATTAATGGATAT 360
Qy 386 Val***ProGluGlyAlaLeu*****PheAsnVal 397
Db 361 GTGATCCAGAGGAGCATTTGATCTCTCAATGTA 396

RESULT 14

US-09-938-842A-2690
Sequence 2690, Application US/09938842A
Patent No. US20030160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2690
LENGTH: 1491
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2690

Alignment Scores:
Pred. No.: 3.85e-71 Length: 1491
Score: 553.00 Matches: 142
Percent Similarity: 50.20% Conservative: 103
Best Local Similarity: 29.10% Mismatches: 205
Query Match: 23.08% Indels: 38
Gaps: 16

US-09-857-581-66 (1-521) x US-09-938-842A-2690 (1-1491)
Qy 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
Db 90 CCACCCGGACCC---CCAGACTTCTATAATTTGAAACTTCACCACTAGATCAAAA 146
Qy 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db 147 ---CCTCATCGTTCGATGTTCAAAATATCCGAACATATGACCTTAAATGCCCTAAAG 203
Qy 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db 204 TTTGGAGCGGTCTACTGTGTGGCATCTACACAGACAGACAGTGTAGGAAAGTCITAAA 263
Qy 95 *****GluAlaThrSerPhe*****ThrArgPheGluThrSerAla***Arg***LeuThr 114
Db 264 ACATTTGACGTAGAAATGTTGTCGCGACCAAAATATGACCTATCCCGCAAGA---GTTAGC 320
Qy 115 TyrAsp-----*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
Db 321 TACATTTAAAGATCTATGCTTTTCTCTATAGCAATATTTGGAGGAGGTACCGAAG 380
Qy 134 LeuIleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
Db 381 ATCAGAGTTGTTGAATCTACACCGCAAAAGGTGCAATCATTTCAACATACAGAAAA 440
Qy 154 GluGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 441 GAAGAAGTTCCAGCCCTCGTTGATTTTCATCAAAAGCTGCTTCATTGGAGAAACCGATT 500
Qy 174 Asp***ThrGluGluLeuLeuLysTyrP***AsnSerThr***SerMetMet***LeuGly 193
Db 501 AACTTGAACAAGAAGTAAATGAACATATCAGGAAGTGTGATTGTAGAGTTGTCATTGTT 560
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeu----- 206
Db 561 ATCAATCTTCAGGAAGTAACTTGAATACATCTATTAAGCATCCTAGACATGAGATTATAAGAT 620
Qy 207 LysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***LeuLysVal 226
Db 621 GAGTTGGTGGGAGTTTTCAGCAGCAGCAGATTACTTT---CCGGTT-----GTT 665
Qy 227 GlyLysTyrGluLysArgIleAspIleLeuAsnLysPheAspProValValGluArg 246
Db 666 GGTAGATCATCGATGAGTACAGGGTTCATAGCAAAATGTGAGAGCTTTTTCAGGCA 725
Qy 247 ValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu*****GluGly 266
Db 726 ATGATGCATTTTTCATCAATCTATAAGCATCCTAGACATGAGATTATTAAGAT 785
Qy 267 Glu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspLysThr***** 285
Db 786 GAT-----ATAATTGACTTCTTCAAGATGAAAGGGGAGAGACTACTACTT 833

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QY 286 --GluLeuLeuIleThrLys*****IleLysGlyLeuValValAsp***PheSerAla 304
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 834 GGGAGATTCTCACTTACCTCGGACCACACCAAGGAATCTTGAGAAATATCTCAAGCT 893
QY 305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro 324
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 894 GGAATAGACACTCTGCACAAAGTTATGACATGGGTGATGACATATTTGATTTCAAACCCA 953
QY 325 ***ValLeu*****AlaArgGluGlu***TySerValVal---GlyLysAsp***Leu 343
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 954 AGAGTTTGAAGAAGCGGCGGAGGTGAGAAAGTGATAAAACACAAAGATGATATC 1013
QY 344 ValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPhe 363
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1014 ATAGAAGAA---GATATAGACGACTCCATATCTGAAATGTTAAAGAAAGCTTT 1070
QY 364 ArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys***Ile 382
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1071 AGGATAACCCACTGTGCCACTTCTAATCCAAAGAGGCTTCAAAAGATGTAAGATC 1130
QY 383 AsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly*** 402
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1131 GGAGTTATATATCCAAAGAAACATGGATCCATCTTAATATATCGGCTATTCATAGG 1190
QY 403 Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr*** 422
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1191 AATCCAAACGTTTGGAAAGATCCAGAAGCTTTATCCCGAGAGGTTTATGGATAGC-- 1247
QY 423 AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPhe 442
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1248 -----CAGATTGACTATAAAGGGTGTGACITTGASTTGTGGCGTTT 1289
QY 443 GlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeu 462
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1290 GGTACGGAAGAGAAATATGCCCTGGTATTGGAATGGGTATGGCTTGCATCTGACT 1349
QY 463 LeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeu 482
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1350 CTTATCAATCTCTTTATCGATTCGATTCGATTCGAGCTT-----CCAGAAGAAATGAAGTA 1403
QY 483 LysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAla 502
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1404 -----GCAGATGTTGATCTTGAGAATCATATGACTTGTGTCTCTAAGAAA 1451
QY 503 HisSerLeuValCysValProLeu 510
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1452 ATCCACTTCAGCTTATCCCGGTC 1475
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RESULT 15

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US-10-142-231-53
; Sequence 53, Application US/10142231
; Publication No. US2003007796A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: CYTOCHROME P450 OXYGENASES AND THEIR USES
; FILE REFERENCE: 62773
; CURRENT APPLICATION NUMBER: US/10/142,231
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/165,250
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 53
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Taxus cuspidata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1539)
; OTHER INFORMATION: "n" equals any oligonucleotide
US-10-142-231-53
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Alignment Scores:

```
Pred. No.: 5,68e-71 Length: 1539
Score: 52.00 Matches: 136
Percent Similarity: 48.80% Conservative: 108
Best Local Similarity: 27.20% Mismatches: 214
Query Match: 23.04% Indels: 42
DB: 9 Gaps: 13

US-09-857-581-66 (1-521) x US-10-142-231-53 (1-1539)

QY 29 LeuArgHisLeuProAsn-----ProProSerPro***ProArgLeuPro 43
    ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||||
Db 106 CTCGCGGCTCATGAACAAATGGAAGATGTCGCCCGGCCCAATTCCA---TGGCCG 162
QY 44 PheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyAla***IleAspLeu 63
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 163 ATCGTGGGAAATCTCCACCAGTTG---GGAAGCTTCCCAACCGTAATCTGGAAGAGCTC 219
QY 64 SerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAla 83
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 GCAAGAAACACGGACCCCATGCTCATGAAATGGGTTCGTTCCCTGCCGTTATCGTT 279
QY 84 SerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***Thr 103
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 TCTTCCTCTGCCATGGCAAAAGAAAGTTCTGAAAATCATGATCTGGTT---TTCGCCAGC 336
QY 104 ArgPheGlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla***** 122
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 337 CGACCCGAAGCGCGCAGAAATACATAGCGTATATTAACAAGATATAGTTTCTCT 396
QY 123 Pro**cLysProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuAsnAla 142
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 397 CCTACGGACCTTACGGAGACAGATGGAAGAAATATCGGTGGTGAATTTGTTGATGCC 456
QY 143 ThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg*** 162
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 457 AGAAGAATCGAGTCGTGAGATCCGTACAGAGGAAGAGGTCTCTGTTATATTCGTTCCG 516
QY 163 Met-----AlaGln***AlaGluAla***LysProLeuAsp*** 175
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 517 GTGTGGGAAGACGACGAGGTCGGCTGCGCTCAATCTGAGCAAGACGCTGCATCC 576
QY 176 ---ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlu 194
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 577 CTTACACGGGACTCATGTTGCAGATCTTTTCCAGTAACGATGACGCGCGGGAATAGCAGC 636
QY 195 AlaGluGluIleArgAspIleAlaArgGluValLeuLysIle**cGlyGluTyrSerLeu 214
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 637 GTCACCCGCCATTAAAGAAATGATGTCGGAGGTCTCTGAGACGCGCGGAGCTTTTAACTT 696
QY 215 ThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAsp 234
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 697 GAGATATTTTCCATGGATGGACTGGATGGATTTGCAGGGTATACAGCGCGCATAGCAG 756
QY 235 AspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***Ile 254
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 757 AAGGCACAGGATATTTCCACGAGGTTCATTACGAAAATATAGACCAACACCCAG----- 810
QY 255 ValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAsp 274
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 811 ---AGGACGAGCGGATGGAGGACACTCAACACCAACAAAGAC-----ATAATTGAC 858
QY 275 ThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile 294
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 859 GCCTGTTGCAGATG-----GAGAACACCGATGGGTCACCATCAATGAAATAATC 912
QY 295 LysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGlu 314
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 913 AAAGCCGTCGTTTGGGTATTTTCTGGCGGAGGAGACGACGCTCCACTACGTTGAA 972
QY 315 TrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu*** 334
    ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 973 TGGCGCATGAGCGCGATGCTTGAACACCTGAGGTGGCCCAAGAAAGTGCAGAGAGATC 1032
```

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QY 335 TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyr 354
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1033 GAATCCGTTGTGGAGAGAGAGGGTGTGAAGAAGATGATCGGGAAGATATGGRATAC 1092
QY 355 IleArgAlaIleValLysGluThrPheArgMetHisProLeuPro---ValValLys 373
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1093 CTGCAATGTGGTGAAGAGACCATGAGATTATATCCGGCGGTGCTTGTCTATCCCG 1152
QY 374 ArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*** 393
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1153 CACGAATCGACCCAGATGTGCTCATGGTACTTCTCTGAAGAACCAGAAATT 1212
QY 394 ***PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu*** 413
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1213 CTCGTTAACGGCGTGGCGGATAGGAAAGATCCAAACGTTGGGATGATGCCCTGGCATTC 1272
QY 414 ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla***LeuAspLeuArg 433
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1273 AAACCAAAAGATTTTG-----GCCAATAATGGGACTTGCAAAAAGGA 1317
QY 434 Gly***HisPheGlnLeuLeuProPheClySerGlyArg***MetCysProGlyVal*** 453
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1318 AAAGAGTTTTCGATATGGTCCCTTGTGGGGAAGAAAGGATGCCCGGGGCAAGC 1377
QY 454 LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGln 473
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1378 ATGGCCGTTGTGACGATGGAAACATGCGTTGGCACAACACTGCTCTCCAGTGGCGC 1437
QY 474 ValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGlu 493
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1438 ATTGAAGGA-----GAGTTGGATATGAGTGAA 1464
QY 494 ArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1465 CGCTTGGCAGCTCCGTCGCAAAAAAAGTCGATCTTTGTGTCTCTCCCAATGGAGGCTA 1524
```

Search completed: June 1, 2003, 03:04:32
Job time : 258 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 26, 2004, 16:59:35 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: us-09-857-581-66
Perfect score: 2396
Sequence: 1 MLELALGLXVLALFXHLRP.....ARSLVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues
Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2396	100.0	521	1	US-09-857-581-2
2	2396	100.0	521	1	US-09-857-581-26
3	2396	100.0	521	1	US-09-857-581-28
4	2396	100.0	521	1	US-09-857-581-30
5	2396	100.0	521	1	US-09-857-581-32
6	2396	100.0	521	1	US-09-857-581-34
7	2396	100.0	521	1	US-09-857-581-36
8	2396	100.0	521	1	US-09-857-581-24
9	2304	96.2	499	1	US-09-857-581-16
10	2304	96.2	499	1	US-09-857-581-18
11	2304	96.2	499	1	US-09-857-581-20
12	2304	96.2	499	1	US-09-857-581-22
13	2304	96.2	499	1	US-09-857-581-40
14	2304	96.2	499	1	US-09-857-581-48
15	2304	96.2	499	1	US-09-857-581-55
16	2304	96.2	499	1	US-09-857-581-57
17	2304	96.2	499	1	US-09-857-581-59
18	2298	95.9	498	1	US-09-857-581-38
19	2293	95.7	498	1	US-09-857-581-61

ALIGNMENTS

RESULT 1
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALFXHLRPPTXAKSALRHPNPSPXPRLPFGHXLKDKLLHYAX 60
DB 1 MLELALGLFVLALFLHRLPTPSAKSALRHPNPSPKPLPFGHHLKDKLLHYAL 60
QY 61 IDLSKKGHPFSXXFGSMPTVASTPELFLQXHEATSFXTFQTSAXKXLYDYXVA 120
DB 61 IDLSKKGHPFSLSFGSMPTVASTPELFLQTHEATSFNTFQTSAIRRLTYDNSVA 120
QY 121 XXPXGPYKXVYRKLIMNDLNNATVNLRLRTOQIRKLRXMAQAEAKPLDXTTELL 180
DB 121 MVPFGYKXVYRKLIMNDLNNATVNLRLRTOQIRKLRXMAQAEAKPLDXTTELL 180
QY 181 KWNSTXSMXKLGEABEIRDIAREVLKIXGYSYTDFTXPLKLVKGVKXKRIIDILNKF 240
DB 181 KWNSTISMMVLGEABEIRDIAREVLKIFGYSYTDFTWPLKLVKGVKXKRIIDILNKF 240
QY 241 DPVVERVVKRRXIVRRKXGEXXGEXSGVXLTLLFAEDETXKIKTKXIKGLVVD 300
DB 241 DPVVERVVKRRXIVRRKXGEXXGEXSGVXLTLLFAEDETXKIKTKXIKGLVVD 300
QY 301 XFSAGXDSTAXTWALAEALNNPKVLXAREEYXSVVGKDXLVDVDTQNLPIRAIVK 360
DB 301 PFSAGDSTAVATWALAEALNNPRVLQKAREEYXSVVGKDLVDVDTQNLPIRAIVK 360
QY 361 ETRFRHPLPVVKKCBECXINGXVAPGALXAFNWWQVGDXXKYWDRSEKPERFLE 420
DB 361 ETRFRHPLPVVKKCBECXINGXVAPGALXAFNWWQVGRDPKYWDRSEKPERFLE 420
QY 421 TXAEGEAXLDRGXHFOLLPFGSGRMXCPGVXLTATGATLLASLIQCPLQVLGPQGG 480
DB 421 TXAEGEAGPLDRGXHFOLLPFGSGRMXCPGVXLTATGATLLASLIQCPLQVLGPQGG 480
QY 481 ILKGDAXVMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
DB 481 ILKGDAXVMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26

		LENGTH: 521					
		TYPE: PRT					
		ORGANISM: Phaseolus aureus					
		US-09-857-581-26					
		Query Match 100.0%; Score 2396; DB 1; Length 521;					
		Best Local Similarity 87.1%; Pred. No. 0;					
		Matches 454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	M L L E A L G L V L A L F X H L R P T P X A S K A L R H L N P S P K P R L P F I G H X H L L K D K L L H Y A X	60	Qy	1	M L L E A L G L V L A L F X H L R P T P X A S K A L R H L N P S P K P R L P F I G H X H L L K D K L L H Y A X	60
Db	1	M L L E A L G L L V L A L F L H L R P T P T A K S K A L R H L N P S P K P R L P F I G H L H L L K D K L L H Y A L	60	Db	1	M L L E A L G L L V L A L F L H L R P T P T A K S K A L R H L N P S P K P R L P F I G H L H L L K D K L L H Y A L	60
Qy	61	I D L S K H G P L F S X F G S M P T V V A S T P E L F K L F L Q X X E A T S F X T R F O T S A X R X L T Y D X X V A	120	Qy	61	I D L S K H G P L F S X F G S M P T V V A S T P E L F K L F L Q X X E A T S F X T R F O T S A X R X L T Y D X X V A	120
Db	61	I D L S K H G P L F S L Y F G S M P T V V A S T P E L F K L F L Q T H E A T S F N T R F O T S A I R R L T Y D S S V A	120	Db	61	I D L S K H G P L F S L Y F G S M P T V V A S T P E L F K L F L Q T H E A T S F N T R F O T S A I R R L T Y D S S V A	120
Qy	121	X X P G P Y W X F V R K L I M N D L L N A T T V N X L R P L R T Q I R K L R X M A Q X A E A K P L D X T B E L L	180	Qy	121	X X P G P Y W X F V R K L I M N D L L N A T T V N X L R P L R T Q I R K L R X M A Q X A E A K P L D X T B E L L	180
Db	121	M V P G P Y W K F V R K L I M N D L L N A T T V N K L R P L R T Q I R K L R V M A Q G A E A Q K P L D L T E E L L	180	Db	121	M V P G P Y W K F V R K L I M N D L L N A T T V N K L R P L R T Q I R K L R V M A Q G A E A Q K P L D L T E E L L	180
Qy	181	K W X N S T S M X M L G E A E E I R D I A R E V L K I X G E Y S L T D F I P L K L K V G K Y E K R I D D I L N K F	240	Qy	181	K W X N S T S M X M L G E A E E I R D I A R E V L K I X G E Y S L T D F I P L K L K V G K Y E K R I D D I L N K F	240
Db	181	K W N S T I S M M L G E A E E I R D I A R E V L K I F G E Y S L T D F I P L K L K V G K Y E K R I D D I L N K F	240	Db	181	K W N S T I S M M L G E A E E I R D I A R E V L K I F G E Y S L T D F I P L K L K V G K Y E K R I D D I L N K F	240
Qy	241	D P V V E R V I K K R X I V R R R X N G E X X E G S G V X L D T L L E F A B D E T X E I K I T K O X I K G L V D	300	Qy	241	D P V V E R V I K K R X I V R R R X N G E X X E G S G V X L D T L L E F A B D E T X E I K I T K O X I K G L V D	300
Db	241	D P V V E R V I K K R E I V R R R K N G E V V E G S G V F L D T L L E F A B D E T T E I K I T K D H I K G L V D	300	Db	241	D P V V E R V I K K R E I V R R R K N G E V V E G S G V F L D T L L E F A B D E T T E I K I T K D H I K G L V D	300
Qy	301	X F S A G X D S T A X T E W A L A E L I N N P X V L X A B E E X Y S V V G K D X L V D E V D T Q N L P Y I R A I V K	360	Qy	301	X F S A G X D S T A X T E W A L A E L I N N P X V L X A B E E X Y S V V G K D X L V D E V D T Q N L P Y I R A I V K	360
Db	301	F F S A G T D S T A V A T E W A L A E L I N N P K V L E K A E E V Y V V G K D R L V D E V D T Q N L P Y I R A I V K	360	Db	301	F F S A G T D S T A V A T E W A L A E L I N N P K V L E K A E E V Y V V G K D R L V D E V D T Q N L P Y I R A I V K	360
Qy	361	E T F R M H P P L P V V K R K X E E C K I N G X V P E G A L X X F N V M Q V G X D X K Y W D R P S E X P E R F L E	420	Qy	361	E T F R M H P P L P V V K R K X E E C K I N G X V P E G A L X X F N V M Q V G X D X K Y W D R P S E X P E R F L E	420
Db	361	E T F R M H P P L P V V K R K T E E C I N G V I P E G A L I L F N V M Q V G R D P K Y W D R P S E F R P E R F L E	420	Db	361	E T F R M H P P L P V V K R K T E E C I N G V I P E G A L I L F N V M Q V G R D P K Y W D R P S E F R P E R F L E	420
Qy	421	T X A G E A X X L D R G H F O L L P F G S G R M C P G V L A T S G X A T L L A S L I Q C F D L O V L G P Q G	480	Qy	421	T X A G E A X X L D R G H F O L L P F G S G R M C P G V L A T S G X A T L L A S L I Q C F D L O V L G P Q G	480
Db	421	T G A G E A R P L D R G H F O L L P F G S G R R M C P G V N L A T S G M A T L L A S L I Q C F D L O V L G P Q G	480	Db	421	T G A G E A R P L D R G H F O L L P F G S G R R M C P G V N L A T S G M A T L L A S L I Q C F D L O V L G P Q G	480
Qy	481	I L K G X D A K V S M E E R A G L T V P R A H S L V C V P L A R I G V A S K L L S	521	Qy	481	I L K G X D A K V S M E E R A G L T V P R A H S L V C V P L A R I G V A S K L L S	521
Db	481	I L K G D A K V S M E E R A G L T V P R A H S L V C V P L A R I G V A S K L L S	521	Db	481	I L K G D A K V S M E E R A G L T V P R A H S L V C V P L A R I G V A S K L L S	521
		RESULT 3					
		US-09-857-581-28					
		Sequence 28, Application US/09857581					
		GENERAL INFORMATION:					
		APPLICANT: E. I. du Pont de Nemours and Company					
		TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase					
		FILE REFERENCE: BB1339 PCT					
		CURRENT APPLICATION NUMBER: US/09/857,581					
		CURRENT FILING DATE: 2001-06-05					
		PRIOR APPLICATION NUMBER: 60/117,769					
		PRIOR FILING DATE: 1999-01-27					
		PRIOR APPLICATION NUMBER: 60/144,783					
		PRIOR FILING DATE: 1999-07-20					
		PRIOR APPLICATION NUMBER: 60/156,094					
		PRIOR FILING DATE: 1999-09-24					
		NUMBER OF SEQ ID NOS: 66					
		SOFTWARE: Microsoft Office 97					
		SEQ ID NO 28					
		LENGTH: 521					
		TYPE: PRT					
		ORGANISM: Phaseolus aureus					
		US-09-857-581-28					
		Query Match 100.0%; Score 2396; DB 1; Length 521;					
		Best Local Similarity 87.1%; Pred. No. 0;					
		Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	M L L E A L G L V L A L F X H L R P T P X A S K A L R H L N P S P K P R L P F I G H X H L L K D K L L H Y A X	60	Qy	1	M L L E A L G L V L A L F X H L R P T P X A S K A L R H L N P S P K P R L P F I G H X H L L K D K L L H Y A X	60
Db	1	M L L E A L G L L V L A L F L H L R P T P T A K S K A L R H L N P S P K P R L P F I G H L H L L K D K L L H Y A L	60	Db	1	M L L E A L G L L V L A L F L H L R P T P T A K S K A L R H L N P S P K P R L P F I G H L H L L K D K L L H Y A L	60
Qy	61	I D L S K H G P L F S X F G S M P T V V A S T P E L F K L F L Q X X E A T S F X T R F O T S A X R X L T Y D X X V A	120	Qy	61	I D L S K H G P L F S X F G S M P T V V A S T P E L F K L F L Q X X E A T S F X T R F O T S A X R X L T Y D X X V A	120
Db	61	I D L S K H G P L F S L Y F G S M P T V V A S T P E L F K L F L Q T H E A T S F N T R F O T S A I R R L T Y D S S V A	120	Db	61	I D L S K H G P L F S L Y F G S M P T V V A S T P E L F K L F L Q T H E A T S F N T R F O T S A I R R L T Y D S S V A	120
Qy	121	X X P G P Y W X F V R K L I M N D L L N A T T V N X L R P L R T Q I R K L R X M A Q X A E A K P L D X T B E L L	180	Qy	121	X X P G P Y W X F V R K L I M N D L L N A T T V N X L R P L R T Q I R K L R X M A Q X A E A K P L D X T B E L L	180

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Db 121 MPPFGYKFKVRLINNDLLNATTNKLRLPTQQLRKELRVVQAQAEAKPLDLTEELL 180
Qy 181 KXNSTXSMXGLGEABEIRDIAREVLKIKGEYSLTDPIPLKXKLVKGYEKRIDDLINKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDLINKF 240
Qy 241 DPVVERVVKRRXIVRRRXNGEXXGXVLDLTLLEFAEDTTEIKITKXIKGLVVD 300
Db 241 DPVVERVVKRRXIVRRRXNGEVVEGEVGVFLDTLLEFAEDTTEIKITKXIKGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVLYXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEVYVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPLPVVVKCKEEXINGXVKEGALXXFNWQVGDXXKYWDPRSEKRPERFLE 420
Db 361 ETRFMHPPLPVVVKCKTECEINGYVPEGALILFNWQVGRDPKYWDPRSEKRPERFLE 420
Qy 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVKXATLASLIQCFLDLQVLGPQOQ 480
Db 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVNLTSGMATLASLIQCFLDLQVLGPQOQ 480
Qy 481 ILKGDAXKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521

RESULT 5
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857, 581
; CURRENT FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLXVLALFXHLRPTTAXSKALRHLNPPSPXPLPFIHGHLLKDLKLLHYAX 60
Db 1 MLELALGLLVLALFLHLRPTTAXSKALRHLNPPSPKPLPFIHGHLLKDLKLLHYAL 60
Qy 61 IDLSKKGHPLFSXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXRXLTYDXVA 120
Db 61 IDLSKKGHPLFSXFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSARLLTYDSSVA 120
Qy 121 XXPGPYKXFKVRKLIMNDLLNATTNKLRLPTQQLRKELRVVQAQAEAKPLDLTEELL 180
Db 121 MYPFGPYKFKVRKLIMNDLLNATTNKLRLPTQQLRKELRVVQAQAEAKPLDLTEELL 180
Qy 181 KXNSTXSMXGLGEABEIRDIAREVLKIXGEYSLTDPIPLKXKLVKGYEKRIDDLINKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDLINKF 240
Qy 241 DPVVERVVKRRXIVRRRXNGEXXGXVLDLTLLEFAEDTTEIKITKXIKGLVVD 300
Db 241 DPVVERVVKRRXIVRRRXNGEVVEGEVGVFLDTLLEFAEDTTEIKITKXIKGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVLYXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEVYVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPLPVVVKCKEEXINGXVKEGALXXFNWQVGDXXKYWDPRSEKRPERFLE 420
Db 361 ETRFMHPPLPVVVKCKTECEINGYVPEGALILFNWQVGRDPKYWDPRSEKRPERFLE 420
Qy 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVKXATLASLIQCFLDLQVLGPQOQ 480
Db 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVNLTSGMATLASLIQCFLDLQVLGPQOQ 480
Qy 481 ILKGDAXKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521
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Db 241 DPVVERVVKRRXIVRRRXNGEVVEGEVGVFLDTLLEFAEDTTEIKITKXIKGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVLYXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEVYVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPLPVVVKCKEEXINGXVKEGALXXFNWQVGDXXKYWDPRSEKRPERFLE 420
Db 361 ETRFMHPPLPVVVKCKTECEINGYVPEGALILFNWQVGRDPKYWDPRSEKRPERFLE 420
Qy 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVKXATLASLIQCFLDLQVLGPQOQ 480
Db 421 TXAEGEAXXLDLRCXHFQLLPFGSGRMCPGVNLTSGMATLASLIQCFLDLQVLGPQOQ 480
Qy 481 ILKGDAXKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVFRAHSLVCVPLARIGVASKLLS 521

RESULT 6
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857, 581
; CURRENT FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLXVLALFXHLRPTTAXSKALRHLNPPSPXPLPFIHGHLLKDLKLLHYAX 60
Db 1 MLELALGLLVLALFLHLRPTTAXSKALRHLNPPSPKPLPFIHGHLLKDLKLLHYAL 60
Qy 61 IDLSKKGHPLFSXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXRXLTYDXVA 120
Db 61 IDLSKKGHPLFSXFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSARLLTYDSSVA 120
Qy 121 XXPGPYKXFKVRKLIMNDLLNATTNKLRLPTQQLRKELRVVQAQAEAKPLDLTEELL 180
Db 121 MYPFGPYKFKVRKLIMNDLLNATTNKLRLPTQQLRKELRVVQAQAEAKPLDLTEELL 180
Qy 181 KXNSTXSMXGLGEABEIRDIAREVLKIXGEYSLTDPIPLKXKLVKGYEKRIDDLINKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLTDPIWPLKHLKVGKYEKRIDDLINKF 240
Qy 241 DPVVERVVKRRXIVRRRXNGEXXGXVLDLTLLEFAEDTTEIKITKXIKGLVVD 300
Db 241 DPVVERVVKRRXIVRRRXNGEVVEGEVGVFLDTLLEFAEDTTEIKITKXIKGLVVD 300
Qy 301 XFSAGXDSAXXTETWALAEIINNXPVLYXAREEYXVVGKDLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAETWALAEIINNPKVLEKAREEVYVVGKDLVDEVDTONLPYIRAIK 360
Qy 361 ETRFMHPPLPVVVKCKEEXINGXVKEGALXXFNWQVGDXXKYWDPRSEKRPERFLE 420
Db 361 ETRFMHPPLPVVVKCKTECEINGYVPEGALILFNWQVGRDPKYWDPRSEKRPERFLE 420
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Qy 421 TXAEGEAXXLDLRCXHFQQLLPGSGRXCMPGVXLTATSGXATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAGEARPLDLRGQHQLLPGSGRRMCPGVNLTATSGMATLLASLIQCFDLQVLGPQGG 480

Qy 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521

RESULT 7
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36

Query Match 100.0%; Score 2396; DB 1; Length 521;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLXVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHXHLKDKLLHYAX 60
Db 1 MLELALGLXVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHXHLKDKLLHYAL 60

Qy 61 IDLSKXHGFLPSXFGSMPTVASTPELFLQXKEATSPXTRFOTSAKRLTYDXXVA 120
Db 61 IDLSKXHGFLPSXFGSMPTVASTPELFLQXKEATSPXTRFOTSAKRLTYDSSVA 120

Qy 121 XXPGPYKXFXVKLIMNDLNNATTVNKLRLPTQOIRKXLRMAQXABAXKPLDXTBELL 180
Db 121 XXPGPYKXFXVKLIMNDLNNATTVNKLRLPTQOIRKXLRMAQXABAXKPLDXTBELL 180

Qy 181 KXNXTSXMMKLGEABEIRDIAREVLYKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
Db 181 KXNXTSXMMKLGEABEIRDIAREVLYKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240

Qy 241 DPVVERVVKRXIIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXXIKGLVVD 300
Db 241 DPVVERVVKRXIIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXXIKGLVVD 300

Qy 301 XFSAGXDSATXATEWALAEELINNPVLYXAREEXYVVGKDXLVDEVDTONLPYIRAIK 360
Db 301 XFSAGXDSATXATEWALAEELINNPVLYXAREEXYVVGKDXLVDEVDTONLPYIRAIK 360

Qy 361 ETRFMHPPPLPVVKRCXBECKXNGXVXPEGALXXFNVMQVXDXKYWRPSEXPFRPLE 420
Db 361 ETRFMHPPPLPVVKRCXBECKXNGXVXPEGALXXFNVMQVXDXKYWRPSEXPFRPLE 420

Qy 421 TXAEGEAXXLDLRCXHFQQLLPGSGRXCMPGVXLTATSGXATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAGEARPLDLRGQHQLLPGSGRRMCPGVNLTATSGMATLLASLIQCFDLQVLGPQGG 480

Qy 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521
```

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RESULT 8
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match 100.0%; Score 2396; DB 1; Length 522;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 454; Conservative 67; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLELALGLXVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHXHLKDKLLHYAX 60
Db 1 MLELALGLXVLALFXHLRPTXAXSKALRHLNPPSPXPRLPFIHGHXHLKDKLLHYAL 60

Qy 61 IDLSKXHGFLPSXFGSMPTVASTPELFLQXKEATSPXTRFOTSAKRLTYDXXVA 120
Db 61 IDLSKXHGFLPSXFGSMPTVASTPELFLQXKEATSPXTRFOTSAKRLTYDSSVA 120

Qy 121 XXPGPYKXFXVKLIMNDLNNATTVNKLRLPTQOIRKXLRMAQXABAXKPLDXTBELL 180
Db 121 XXPGPYKXFXVKLIMNDLNNATTVNKLRLPTQOIRKXLRMAQXABAXKPLDXTBELL 180

Qy 181 KXNXTSXMMKLGEABEIRDIAREVLYKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
Db 181 KXNXTSXMMKLGEABEIRDIAREVLYKXGEVSLTDFIXPLKXKLVGKYEKRIIDILNKF 240

Qy 241 DPVVERVVKRXIIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXXIKGLVVD 300
Db 241 DPVVERVVKRXIIVRRXNGEXXGEXGVXLDTLLEFADETXEIKITKXXIKGLVVD 300

Qy 301 XFSAGXDSATXATEWALAEELINNPVLYXAREEXYVVGKDXLVDEVDTONLPYIRAIK 360
Db 301 XFSAGXDSATXATEWALAEELINNPVLYXAREEXYVVGKDXLVDEVDTONLPYIRAIK 360

Qy 361 ETRFMHPPPLPVVKRCXBECKXNGXVXPEGALXXFNVMQVXDXKYWRPSEXPFRPLE 420
Db 361 ETRFMHPPPLPVVKRCXBECKXNGXVXPEGALXXFNVMQVXDXKYWRPSEXPFRPLE 420

Qy 421 TXAEGEAXXLDLRCXHFQQLLPGSGRXCMPGVXLTATSGXATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAGEARPLDLRGQHQLLPGSGRRMCPGVNLTATSGMATLLASLIQCFDLQVLGPQGG 480

Qy 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGDAXKSMERAGLTVBRAHSLVCVPLARIGVASKILLS 521

RESULT 9
US-09-857-581-16
; Sequence 16, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
```



```
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
; US-09-857-581-16

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAKSKALRHLNPNPSPXPRLPFFIGHXHLKDKLLHYAXIDLKSKGGLPFSXX 74
DB 1 FLHLRPTSAKSKALRHLNPNPSPXPRLPFFIGHLHLKDKLLHYALIDLKSKGGLPFSLS 60

QY 75 FGSMTVVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVAXXPXGYWYXVVRKL 134
DB 61 FGSMTVVASTPELFLQTHEATSFNTRFQTSAXRXLTYDLSVAMVFFGYWYXVVRKL 120

QY 135 IMNDLLNATTNKLRLPTQIRKRLXMAQXAEAKPLDXTTEILLKXNXTXSMMLGE 194
DB 121 IMNDLLNATTNKLRLPTQIRKRLVMAQAEAKPLDXTTEILLKXNXTXSMMLGE 180

QY 195 ABEIRDIAREVLKXGEYSLTDFTXPLKXKLVGYEKRIDDLINKFPDVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLTDFTWPLKXKLVGYEKRIDDLINKFPDVERVVKRREI 240

QY 255 VRRXNGEXXGEXSGVLDLTLLEFAEDTETXIKITKXIKGLVVDXFSAGXDSTAXTE 314
DB 241 VRRXNGEVVEGSGVLDLTLLEFAEDTETIKITKHIGLVVDXFSAGIDSTAVATE 300

QY 315 WALAEILNPNVLXAXREEXSVVQKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVVR 374
DB 301 WALAEILNPNVLQXAREEVSXVQKRLVDEVTQNLPIYRAIVKETFMRHPPPLPVVVR 360

QY 375 KCXEECXINGXVXPEGALXXFNVMQVGDXXKYWDPSXERPERFLETXAEGEAXXLDLRG 434
DB 361 KCTECEEINGVYIPGALVLFNVMQVGRDPKYWDPSERPERFLETGAEGEARFJDLRG 420

QY 435 XHFQLLPFGSGRXXMCPGVXKATLSGXATLIASLIQCFDLQVLGPOGQILKGDAXVSMER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLIASLIQCFDLQVLGPOGQILKGDAXVSMER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 11
US-09-857-581-20
; Sequence 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
; US-09-857-581-20

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
; US-09-857-581-16

Query Match      96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAKSKALRHLNPNPSPXPRLPFFIGHXHLKDKLLHYAXIDLKSKGGLPFSXX 74
DB 1 FLHLRPTSAKSKALRHLNPNPSPXPRLPFFIGHLHLKDKLLHYALIDLKSKGGLPFSLS 60

QY 75 FGSMTVVASTPELFLQXKXATSFTRFQTSAXRXLTYDXXVAXXPXGYWYXVVRKL 134
DB 61 FGSMTVVASTPELFLQTHEATSFNTRFQTSAXRXLTYDLSVAMVFFGYWYXVVRKL 120

QY 135 IMNDLLNATTNKLRLPTQIRKRLXMAQXAEAKPLDXTTEILLKXNXTXSMMLGE 194
DB 121 IMNDLLNATTNKLRLPTQIRKRLVMAQAEAKPLDXTTEILLKXNXTXSMMLGE 180

QY 195 ABEIRDIAREVLKXGEYSLTDFTXPLKXKLVGYEKRIDDLINKFPDVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLTDFTWPLKXKLVGYEKRIDDLINKFPDVERVVKRGI 240

QY 255 VRRXNGEXXGEXSGVLDLTLLEFAEDTETXIKITKXIKGLVVDXFSAGXDSTAXTE 314
DB 241 VRRXNGEVVEGSGVLDLTLLEFAEDTETIKITKHIGLVVDXFSAGIDSTAVATE 300

QY 315 WALAEILNPNVLXAXREEXSVVQKXLDVDEVTQNLPIYRAIVKETFMRHPPPLPVVVR 374
DB 301 WALAEILNPNVLQXAREEVSXVQKRLVDEVTQNLPIYRAIVKETFMRHPPPLPVVVR 360

QY 375 KCXEECXINGXVXPEGALXXFNVMQVGDXXKYWDPSXERPERFLETXAEGEAXXLDLRG 434
DB 361 KCTECEEINGVYIPGALVLFNVMQVGRDPKYWDPSERPERFLETGAEGEARFJDLRG 420

QY 435 XHFQLLPFGSGRXXMCPGVXKATLSGXATLIASLIQCFDLQVLGPOGQILKGDAXVSMER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTSGMATLIASLIQCFDLQVLGPOGQILKGDAXVSMER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-18
; Sequence 18, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
```

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QY 15 FXHLRPTXAKSKALRHLNPPSPXPRLPFIQHXHLLKDKLLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLLHYALIDLKSKHGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTSTISNMVLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDFIWPJLXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314
DB 241 VRRXNGEXVEGEASGVFLDTLLEFADETXEIKITKQIKGLVVDVFSAGTDSVATE 300
QY 315 WALAELINNPVXXAREEYXVVGKDXLVDVDTQNLPIYIRAIIVKETFMRHPPPLPVVXR 374
DB 301 WALAELINNPVXLEKAREEYXVVGKDXLVDVDTQNLPIYIRAIIVKETFMRHPPPLPVVXR 360
QY 375 KCXECXINGVXVPEGALXXFNWVGDXKXVWDRPSEXPXRPFLTXAEGAXXLDLGR 434
DB 361 KCTECEINGVXVPEGALVFNWVGDRPKYWDPRSEXPXRPFLTXAEGEAGPLDLRG 420
QY 435 XHFQLLPFGSGRXCPCGVXKATLSGXTATLASLIQCFDLQVLGPGQOILKGDAXVMEER 494
DB 421 QHFQLLPFGSGRXCPCGVNLTSGWATLASLIQCFDLQVLGPGQOILKGDAXVMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
```

```
RESULT 12
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-22
```

```
Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTXAKSKALRHLNPPSPXPRLPFIQHXHLLKDKLLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLLHYALIDLKSKHGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
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QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTSTISNMVLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDFIWPJLXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314
DB 241 VRRXNGEXVEGEASGVFLDTLLEFADETXEIKITKQIKGLVVDVFSAGTDSVATE 300
QY 315 WALAELINNPVXXAREEYXVVGKDXLVDVDTQNLPIYIRAIIVKETFMRHPPPLPVVXR 374
DB 301 WALAELINNPVXLEKAREEYXVVGKDXLVDVDTQNLPIYIRAIIVKETFMRHPPPLPVVXR 360
QY 375 KCXECXINGVXVPEGALXXFNWVGDXKXVWDRPSEXPXRPFLTXAEGAXXLDLGR 434
DB 361 KCTECEINGVXVPEGALVFNWVGDRPKYWDPRSEXPXRPFLTXAEGEAGPLDLRG 420
QY 435 XHFQLLPFGSGRXCPCGVXKATLSGXTATLASLIQCFDLQVLGPGQOILKGDAXVMEER 494
DB 421 RHQFLLPFGSGRXCPCGVNLTSGWATLASLIQCFDLQVLGPGQOILKGDAXVMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
```

```
RESULT 13
US-09-857-581-40
; Sequence 40, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Trifolium repens
US-09-857-581-40
```

```
Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;
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QY 15 FXHLRPTXAKSKALRHLNPPSPXPRLPFIQHXHLLKDKLLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIQHPHLLKDKLLHYALIDLKSKHGPLFSLY 60
QY 75 FGSMTPTVASTPELFLKFLQXKEATSFXTRFQTSAXRLTYDXXVAXXPXGYPWKFVRKL 134
DB 61 FGSMTPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLLNATTVNKLRLPRTQOIRKRLXMAQXAEAKPLDXTBELLKXNXTXSMXKLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMQAQAEAKPLDXTBELLKXNXTSTISNMVLGE 180
QY 195 ABEIRDIAREVLKIXGEYSLTDFIXPLKXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDFIWPJLXKLVKGYEKRIDDIILNKFPDVPVERVIKRRXI 240
QY 255 VRRXNGEXXGEXSGVXLDLTLLEFADETXEIKITKXIKGLVVDVFSAGXDSTAXTE 314
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Db 241 VRRKNGEVEGEASGVFLDTLLEFAEDTWEIKITKEQIKGLVVDFFSAGTDSVATE 300
Qy 315 WALAEILNNPVXVAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 374
Db 301 WALAEILNNPVQVKAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 360
Qy 375 KCXEECXINGVXVPEGALXFNVMQVGDXXKYWDRPSEXPREFLETXAEGEAXXLDLRG 434
Db 361 KCTEBCEINGVYIPEGALVFNVMQVGRDPKYWDRPSEXPREFLETGAEGAGPLDLRG 420
Qy 435 XHFOLLPGSGRGMCPGVXKATLASLIQCFDQVLQVLPQGOILKGDAXKYSMEER 494
Db 421 QHFOLLPGSGRGMCPGVNLTATSGMATLLASLIQCFDQVLQVLPQGOILKGDAXYSMEER 480
Qy 495 AGLTVBRAHSLVCVPLARI 513
Db 481 AGLTVBRAHSLVCVPLARI 499

RESULT 14
US-09-857-581-48
; Sequence 48, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR APPLICATION NUMBER: 2001-06-05
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 48
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-48

Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

Qy 15 FXHLRPTXAXSKALRHLPNPPSPKPRLPFFIGHXHLKDKLLHYAXIDLKXHGPLFSXX 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLELLKDKLLHYALIDLKXHGPLFSLY 60
Qy 75 FGSMTVVASTPELFLQXKEATSFXTRFOTSAIRLTYDSSVAVVPGPYWKFVRKL 134
Db 61 FGSMTVVASTPELFLQTHEATSFNTRFOTSAIRLTYDSSVAVVPGPYWKFVRKL 120
Qy 135 IMNDLLNATVXKLRLPTQIRKFLRWQAQAEAKPLDTEELLKXNSTXSMMLGE 194
Db 121 IMNDLLNATVXKLRLPTQIRKFLRWQAQAEAKPLDTEELLKXNSTXSMMLGE 180
Qy 195 ABEIRDIAREVLIKXGEYSLDTDFIXPLKXKLVGKYEKIDDIILNKFPVVERVVKRXXI 254
Db 181 ABEIRDIAREVLIKXGEYSLDTDFIWLKXKLVGKYEKIDDIILNKFPVVERVVKRREI 240
Qy 255 VRRXNGEXXEGXSGVXLDLTLLEFAEDTWEIKITKXIKGLVVDXFSAGXDSAXXTE 314
Db 241 VRRXNGEXXEGXSGVXLDLTLLEFAEDTWEIKITKXIKGLVVDXFSAGTDSVATE 300
Qy 315 WALAEILNNPVXVAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 374
Db 301 WALAEILNNPVQVKAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 360
Qy 375 KCXEECXINGVXVPEGALXFNVMQVGDXXKYWDRPSEXPREFLETXAEGEAXXLDLRG 434
Db 361 KCTEBCEINGVYIPEGALVFNVMQVGRDPKYWDRPSEXPREFLETGAEGAGPLDLRG 420
Qy 435 XHFOLLPGSGRGMCPGVXKATLASLIQCFDQVLQVLPQGOILKGDAXKYSMEER 494
Db 421 QHFOLLPGSGRGMCPGVNLTATSGMATLLASLIQCFDQVLQVLPQGOILKGDAXYSMEER 480
Qy 495 AGLTVBRAHSLVCVPLARI 513
Db 481 AGLTVBRAHSLVCVPLARI 499
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Db 361 KCTEBCEINGVYIPEGALVFNVMQVGRDPKYWDRPSEXPREFLETGAEGAGPLDLRG 420
Qy 435 XHFOLLPGSGRGMCPGVXKATLASLIQCFDQVLQVLPQGOILKGDAXKYSMEER 494
Db 421 QHFOLLPGSGRGMCPGVNLTATSGMATLLASLIQCFDQVLQVLPQGOILKGDAXYSMEER 480
Qy 495 AGLTVBRAHSLVCVPLARI 513
Db 481 AGLTVBRAHSLVCVPLARI 499

RESULT 15
US-09-857-581-55
; Sequence 55, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR APPLICATION NUMBER: 2001-06-05
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lupinus albus
US-09-857-581-55

Query Match 96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

Qy 15 FXHLRPTXAXSKALRHLPNPPSPKPRLPFFIGHXHLKDKLLHYAXIDLKXHGPLFSXX 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLELLKDKLLHYALIDLKXHGPLFSLY 60
Qy 75 FGSMTVVASTPELFLQXKEATSFXTRFOTSAIRLTYDSSVAVVPGPYWKFVRKL 134
Db 61 FGSMTVVASTPELFLQTHEATSFNTRFOTSAIRLTYDSSVAVVPGPYWKFVRKL 120
Qy 135 IMNDLLNATVXKLRLPTQIRKFLRWQAQAEAKPLDTEELLKXNSTXSMMLGE 194
Db 121 IMNDLLNATVXKLRLPTQIRKFLRWQAQAEAKPLDTEELLKXNSTXSMMLGE 180
Qy 195 ABEIRDIAREVLIKXGEYSLDTDFIXPLKXKLVGKYEKIDDIILNKFPVVERVVKRXXI 254
Db 181 ABEIRDIAREVLIKXGEYSLDTDFIWLKXKLVGKYEKIDDIILNKFPVVERVVKRREI 240
Qy 255 VRRXNGEXXEGXSGVXLDLTLLEFAEDTWEIKITKXIKGLVVDXFSAGXDSAXXTE 314
Db 241 VRRXNGEXXEGXSGVXLDLTLLEFAEDTWEIKITKXIKGLVVDXFSAGTDSVATE 300
Qy 315 WALAEILNNPVXVAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 374
Db 301 WALAEILNNPVQVKAREEYSVVGKDXLVDEVDTQNLPIYRAIVKETFHMHPLPVVKR 360
Qy 375 KCXEECXINGVXVPEGALXFNVMQVGDXXKYWDRPSEXPREFLETXAEGEAXXLDLRG 434
Db 361 KCTEBCEINGVYIPEGALVFNVMQVGRDPKYWDRPSEXPREFLETGAEGAGPLDLRG 420
Qy 435 XHFOLLPGSGRGMCPGVXKATLASLIQCFDQVLQVLPQGOILKGDAXKYSMEER 494
Db 421 QHFOLLPGSGRGMCPGVNLTATSGMATLLASLIQCFDQVLQVLPQGOILKGDAXYSMEER 480
Qy 495 AGLTVBRAHSLVCVPLARI 513
Db 481 AGLTVBRAHSLVCVPLARI 499
```

```
RESULT 16
US-09-857-581-57
; Sequence 57, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-57

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLHYAXIDLKXGGLPFSXX 74
DB 1 FLHLRPTPTAKSKALRHLPNPPSPKRLPFFIGHLHLKDLHYALIDLKXGGLPFSLY 60
QY 75 FGSMPTVAVASTPELFKFLQXAEATSFTRFQTSAXRLTYDXXVAXXPXGPMXFKVRL 134
DB 61 FGSMPTVAVASTPELFKFLQTHAATSFTRFQTSAIRRLTYDSSVAMVPFGPMXFKVRL 120
QY 135 IMNDLNNATTVNKLRLPRTQIRKLRMAQXABAKPDLXTELLKXNXTXSMXKLG 194
DB 121 IMNDLNNATTVNKLRLPRTQIRKLRVMAQGAQKPLDLTELLKXNXTXSMXKLG 180
QY 195 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRREI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXKIGLVVDXFSAGXDSTAXTE 314
DB 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETIKTKDHIKGLVVDFFSAGTDSAVATE 300
QY 315 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
DB 301 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGXVXPGALXFNWQVGDXXKYWDPSXRPXRPFLXETXAGEXAXLDRG 434
DB 361 KCTEECEINGVYIPGALILFNWQVGRDPKYWDPSRFRPERFLETGAGEARPLDRG 420
QY 435 XHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 494
DB 421 QHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 17
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLHYAXIDLKXGGLPFSXX 74
DB 1 FLHLRPTPTAKSKALRHLPNPPSPKRLPFFIGHLHLKDLHYALIDLKXGGLPFSLY 60
QY 75 FGSMPTVAVASTPELFKFLQXAEATSFTRFQTSAXRLTYDXXVAXXPXGPMXFKVRL 134
DB 61 FGSMPTVAVASTPELFKFLQTHAATSFTRFQTSAIRRLTYDSSVAMVPFGPMXFKVRL 120
QY 135 IMNDLNNATTVNKLRLPRTQIRKLRMAQXABAKPDLXTELLKXNXTXSMXKLG 194
DB 121 IMNDLNNATTVNKLRLPRTQIRKLRVMAQGAQKPLDLTELLKXNXTXSMXKLG 180
QY 195 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRREI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXKIGLVVDXFSAGXDSTAXTE 314
DB 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETIKTKDHIKGLVVDFFSAGTDSAVATE 300
QY 315 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
DB 301 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGXVXPGALXFNWQVGDXXKYWDPSXRPXRPFLXETXAGEXAXLDRG 434
DB 361 KCTEECEINGVYIPGALILFNWQVGRDPKYWDPSRFRPERFLETGAGEARPLDRG 420
QY 435 XHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 494
DB 421 QHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 18
US-09-857-581-38
; Sequence 38, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 38
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-38

Query Match          96.2%; Score 2304; DB 1; Length 499;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 433; Conservative 66; Mismatches 0; Indels 0; Gaps 0;

QY 15 FXHLRPTPXAXSKALRHLPNPPSPXPRLPFFIGHXHLKDLHYAXIDLKXGGLPFSXX 74
DB 1 FLHLRPTPTAKSKALRHLPNPPSPKRLPFFIGHLHLKDLHYALIDLKXGGLPFSLY 60
QY 75 FGSMPTVAVASTPELFKFLQXAEATSFTRFQTSAXRLTYDXXVAXXPXGPMXFKVRL 134
DB 61 FGSMPTVAVASTPELFKFLQTHAATSFTRFQTSAIRRLTYDSSVAMVPFGPMXFKVRL 120
QY 135 IMNDLNNATTVNKLRLPRTQIRKLRMAQXABAKPDLXTELLKXNXTXSMXKLG 194
DB 121 IMNDLNNATTVNKLRLPRTQIRKLRVMAQGAQKPLDLTELLKXNXTXSMXKLG 180
QY 195 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRXXI 254
DB 181 ABEIRDIAREVLKXGEYSLDTFIPXPLKXKVGKYEKIDIDILNKFPVVERVVKRREI 240
QY 255 VRRRXNGEXXGEXSGVLDLTLLEPAEDTETXIKTKXKIGLVVDXFSAGXDSTAXTE 314
DB 241 VRRRXNGEVVEGSGVLDLTLLEPAEDTETIKTKDHIKGLVVDFFSAGTDSAVATE 300
QY 315 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 374
DB 301 WALAELINNPXVXXAREEYSVVGKDLVDEVDTONLPYIRAIVKETFRMHPPPLPVVKR 360
QY 375 KCXEECXINGXVXPGALXFNWQVGDXXKYWDPSXRPXRPFLXETXAGEXAXLDRG 434
DB 361 KCTEECEINGVYIPGALILFNWQVGRDPKYWDPSRFRPERFLETGAGEARPLDRG 420
QY 435 XHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 494
DB 421 QHFQLLPFGSGRMCPCGYKXATLLASLQCFDLQVLGPGQQLKXGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
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OM protein - protein search, using sw model

Run on: March 1, 2004, 07:06:46 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: af135484pep
Perfect score: 2679
Sequence: 1 MLELALGLLVIALFLHLP.....AHSIVCVPLARIGVASKLS 521

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues
Total number of hits satisfying chosen parameters: 19

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2667	99.6	521	1	US-09-857-581-26
2	2667	99.6	522	1	US-09-857-581-24
3	2665	99.5	521	1	US-09-857-581-28
4	2665	99.5	521	1	US-09-857-581-30
5	2665	99.5	521	1	US-09-857-581-34
6	2652	99.0	521	1	US-09-857-581-32
7	2614	97.6	521	1	US-09-857-581-2
8	2596	96.9	521	1	US-09-857-581-36
9	2563	95.7	499	1	US-09-857-581-59
10	2554	95.3	499	1	US-09-857-581-22
11	2553	95.3	499	1	US-09-857-581-48
12	2548	95.1	499	1	US-09-857-581-18
13	2544	95.0	499	1	US-09-857-581-55
14	2539	94.8	499	1	US-09-857-581-57
15	2528	94.4	499	1	US-09-857-581-40
16	2525	94.3	499	1	US-09-857-581-61
17	2519	94.0	499	1	US-09-857-581-20
18	2498	93.2	499	1	US-09-857-581-16
19	2473	92.3	498	1	US-09-857-581-38

ALIGNMENTS

RESULT 1
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT FILING DATE: 2001-06-05
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
; US-09-857-581-26

Query Match 99.6%; Score 2667; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVIALFLHLPPTAKSKALRHLPNPPSPKPRLPFFIGHLLKDLHVAL 60
Db 1 MLELALGLLVIALFLHLPPTAKSKALRHLPNPPSPKPRLPFFIGHLLKDLHVAL 60
QY 61 IDLSKKHGPLFSLYFGSMPTVASTPELFLKFLQTHEATSFNTRPQTSAIRRLTYDSSVA 120
Db 61 IDLSKKHGPLFSLYFGSMPTVASTPELFLKFLQTHEATSFNTRPQTSAIRRLTYDSSVA 120
QY 121 MYPFGPYKFKVRLKMDLLNATTVNKLRLPTQIRKFLRVMAQGAQKPLDLTEILL 180
Db 121 MYPFGPYKFKVRLKMDLLNATTVNKLRLPTQIRKFLRVMAQGAQKPLDLTEILL 180
QY 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLDFIWPFLKHLKVGKYEKIDILNKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSLDFIWPFLKHLKVGKYEKIDILNKF 240
QY 241 DPVVERVIKRRREIVRRKNGEVVSGVGLDTLLLEFADETHWEIKTKDHKIGLVVD 300
Db 241 DPVVERVIKRRREIVRRKNGEVVSGVGLDTLLLEFADETHWEIKTKDHKIGLVVD 300
QY 301 FFSAGTDSAVATEWALAEILNPKVLEKAREVSVVGKDLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEILNPKVLEKAREVSVVGKDLVDEVDTONLPYIRAIYK 360
QY 361 ETRFMHPPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWRPSPFRERFLE 420
Db 361 ETRFMHPPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWRPSPFRERFLE 420
QY 421 TGAEGEAGPLDLRGQHFLPFGSGRMCPCGVNLTSGMATLLASLIQCDFIQLVGPQQ 480
Db 421 TGAEGEAGPLDLRGQHFLPFGSGRMCPCGVNLTSGMATLLASLIQCDFIQLVGPQQ 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLS 521

RESULT 2
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT FILING DATE: 2001-06-05
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match          99.6%; Score 2667; DB 1; Length 522;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60
Dd 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60

QY 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120
Dd 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Dd 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

QY 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEVSLTDFIWLPLKHLKVGKYEKRIIDILNKF 240
Dd 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEVSLTDFIWLPLKHLKVGKYEKRIIDILNKF 240

QY 241 DPVVERVIKKREIIVRRKNGEVEVSGVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300
Dd 241 DPVVERVIKKREIIVRRKNGEVEVSGVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300

QY 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360
Dd 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360

QY 361 ETRFMHPPLPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Dd 361 ETRFMHPPLPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFDLQVLGPOGQ 480
Dd 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFDLQVLGPOGQ 480

QY 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Dd 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 4
US-09-857-581-30
; Sequence 30, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-30

Query Match          99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60
Dd 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60

QY 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120
Dd 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Dd 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

Query Match          99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60
Dd 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60

QY 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120
Dd 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Dd 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match          99.6%; Score 2667; DB 1; Length 522;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60
Dd 1 MLELALGLLVLFHRLRPTPTAKSKALRHLNPPSPKPLPFIHGHLLHLLKOKLLHYAL 60

QY 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120
Dd 61 IDLSKXHGFLPSLYFGSMPTVASTPELFLQLOTHEATSFNTRFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180
Dd 121 MYPFGPYKFKVRKLIIMNDLLNATTNKLRLPTQIRKFLRVMAQGAQAQKPLDTEELL 180

QY 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEVSLTDFIWLPLKHLKVGKYEKRIIDILNKF 240
Dd 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEVSLTDFIWLPLKHLKVGKYEKRIIDILNKF 240

QY 241 DPVVERVIKKREIIVRRKNGEVEVSGVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300
Dd 241 DPVVERVIKKREIIVRRKNGEVEVSGVFLDTLLEFAEDTMEIKITKHIGKGLVVD 300

QY 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360
Dd 301 FFSAGTDSAVATEWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360

QY 361 ETRFMHPPLPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Dd 361 ETRFMHPPLPVVKRKCTECEEINGVYIPGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFDLQVLGPOGQ 480
Dd 421 TGAEGEAGPLDLRGQHFQLLPFGSGRMCPCGVNLTSGMATLLASLIQCFDLQVLGPOGQ 480

QY 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Dd 481 ILKGGDAKYSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 3
US-09-857-581-28
; Sequence 28, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 28
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-28

Query Match          99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 121 MPPFGPYKKEVRKLIIMNDLLNATVVKLRPLRTQQIRKFLRVVAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 5
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 99.5%; Score 2665; DB 1; Length 521;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 519; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLAFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKDKLLHYAL 60
Db 1 MLELALGLLVLAFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKDKLLHYAL 60
Qy 61 IDLSKXGGLPFLSYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKXGGLPFLSYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPFGPYKKEVRKLIIMNDLLNATVVKLRPLRTQQIRKFLRVVAQGAQKPLDLTEELL 180
Db 121 MPPFGPYKKEVRKLIIMNDLLNATVVKLRPLRTQQIRKFLRVVAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
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Db 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Db 421 TGAEGEAGPLDLRGQHFLQFPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 6
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR FILING DATE: 1999-01-27
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 99.0%; Score 2652; DB 1; Length 521;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 517; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLAFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKDKLLHYAL 60
Db 1 MLELALGLLVLAFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKDKLLHYAL 60
Qy 61 IDLSKXGGLPFLSYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKXGGLPFLSYFGSMPTVVASTPELFLQTHREATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPFGPYKKEVRKLIIMNDLLNATVVKLRPLRTQQIRKFLRVVAQGAQKPLDLTEELL 180
Db 121 MPPFGPYKKEVRKLIIMNDLLNATVVKLRPLRTQQIRKFLRVVAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGYSLTDPINFLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVVEGVSGLVDTLLLEFAEDETMEIKITKDHIKGLVVD 300
Qy 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Db 301 FFSAGTDSAVATEWALAEIINNPKVLEKAREEVYVVGKDRLVDEVDTONLPYIRAIYK 360
Qy 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTEECINGVYIPEGALILFNWQVGRDPKYWDRPSEFRPERFLE 420
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QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
DB 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
DB 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 7
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2

Query Match 97.6%; Score 2614; DB 1; Length 521;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 507; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPRTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHYAL 60
DB 1 MLELALGLFVLALFHLRPTPSAKSKALRHLNPPSPKPLPFIHLLKDKLLHYAL 60

QY 61 IDLSKKGPLFSLYFGSMPTVASTPELTKLFLQTHEATSFNTFQTSAIRRLTYDSSVA 120
DB 61 IDLSKKGPLFSLYFGSMPTVASTPELTKLFLQTHEATSFNTFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAEAQKPLDTEELL 180
DB 121 MYPFGPYKFKVRLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAEAQKPLDTEELL 180

QY 181 KWTNSTISMMMLGEAEIRDIAREVLTDFWPLKHLKVGKYEKRIDDILNKF 240
DB 181 KWTNSTISMMMLGEAEIRDIAREVLTDFWPLKHLKVGKYEKRIDDILNKF 240

QY 241 DPWVERVIKKREIVRRKNGEVVEGSGVFLDTLLEFADETMETIKTDHIKGLVVD 300
DB 241 DPWVERVIKKREIVRRKNGEVVEGSGVFLDTLLEFADETMETIKTDHIKGLVVD 300

QY 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360
DB 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360

QY 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
DB 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
DB 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
DB 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
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RESULT 8
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36

Query Match 96.9%; Score 2596; DB 1; Length 521;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 502; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPRTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHYAL 60
DB 1 MLELALGLFVLALFHLRPTPSAKSKALRHLNPPSPKPLPFIHLLKDKLLHYAL 60

QY 61 IDLSKKGPLFSLYFGSMPTVASTPELTKLFLQTHEATSFNTFQTSAIRRLTYDSSVA 120
DB 61 IDLSKKGPLFSLYFGSMPTVASTPELTKLFLQTHEATSFNTFQTSAIRRLTYDSSVA 120

QY 121 MYPFGPYKFKVRLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAEAQKPLDTEELL 180
DB 121 MYPFGPYKFKVRLIMNDLLNATTNKLRLPTQOIRKFLVMAQSAEAQKPLDTEELL 180

QY 181 KWTNSTISMMMLGEAEIRDIAREVLTDFWPLKHLKVGKYEKRIDDILNKF 240
DB 181 KWTNSTISMMMLGEAEIRDIAREVLTDFWPLKHLKVGKYEKRIDDILNKF 240

QY 241 DPWVERVIKKREIVRRKNGEVVEGSGVFLDTLLEFADETMETIKTDHIKGLVVD 300
DB 241 DPWVERVIKKREIVRRKNGEVVEGSGVFLDTLLEFADETMETIKTDHIKGLVVD 300

QY 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360
DB 301 FFSAGTDSATAWALAEELINNPVKLEKAREEVSVVVKORLVDVDTQNLPIYRAIVK 360

QY 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
DB 361 ETRFRHPPLPVVKRKTCECEINGVIPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420

QY 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480
DB 421 TGAEGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPQG 480

QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
DB 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
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RESULT 9
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
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; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match      95.7%; Score 2563; DB 1; Length 499;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 495; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 15 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIHLLKDKLLHYALIDLSKKGHPFLSLY 74
Db 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIHLLKDKLLHYALIDLSKKGHPFLSLY 60

Qy 75 FGSMTVVASTPELFKLFLOTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 134
Db 61 FGSMTVVASTPELFKLFLOTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 120

Qy 135 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTELLKWTNSTISMMMLGE 194
Db 121 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTELLKWTNSTISMMMLGE 180

Qy 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 254
Db 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 240

Qy 255 VRRKNGEVEGEVSGVFLDTLLFEADETWEIKITKDHIKGLVDFPSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLFEADETWEIKITKDHIKGLVDFPSAGTDSAVATE 300

Qy 315 WALAEILNNPKVLEKAREEVSVVGKDLVDEVDTONLPYIRALVKETFRMHPPPLPVYKR 374
Db 301 WALAEILNNPKVLEKAREEVSVVGKDLVDEVDTONLPYIRALVKETFRMHPPPLPVYKR 360

Qy 375 KCTEECEINGVIVEGALLILFNVMQVGRDPKYWDRPSEFRPERFLETGAGEAGPLDLRG 434
Db 361 KCTEECEINGVIVEGALLILFNVMQVGRDPKYWDRPSEFRPERFLETGAGEAGPLDLRG 420

Qy 435 QHFOLLPGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 494
Db 421 QHFOLLPGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 480

Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97

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; SEQ ID NO 22
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-22

Query Match      95.3%; Score 2554; DB 1; Length 499;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 494; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 15 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIHLLKDKLLHYALIDLSKKGHPFLSLY 74
Db 1 FLHLRPTPTAKSKALRHLNPPSPKPRLPFIHLLKDKLLHYALIDLSKKGHPFLSLY 60

Qy 75 FGSMTVVASTPELFKLFLOTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 134
Db 61 FGSMTVVASTPELFKLFLOTHETATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 120

Qy 135 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTELLKWTNSTISMMMLGE 194
Db 121 IMNDLLNATTNKLRLPTQOIRKFLRVMAQGAQKPLDLTELLKWTNSTISMMMLGE 180

Qy 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 254
Db 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKIDIDILNKFPDPPVERVVKRREI 240

Qy 255 VRRKNGEVEGEVSGVFLDTLLFEADETWEIKITKDHIKGLVDFPSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLFEADETWEIKITKDHIKGLVDFPSAGTDSAVATE 300

Qy 315 WALAEILNNPKVLEKAREEVSVVGKDLVDEVDTONLPYIRALVKETFRMHPPPLPVYKR 374
Db 301 WALAEILNNPKVLEKAREEVSVVGKDLVDEVDTONLPYIRALVKETFRMHPPPLPVYKR 360

Qy 375 KCTEECEINGVIVEGALLILFNVMQVGRDPKYWDRPSEFRPERFLETGAGEAGPLDLRG 434
Db 361 KCTEECEINGVIVEGALLILFNVMQVGRDPKYWDRPSEFRPERFLETGAGEAGPLDLRG 420

Qy 435 QHFOLLPGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 494
Db 421 QHFOLLPGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPGQQLKGGDAKVSMEER 480

Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 11
US-09-857-581-48
; Sequence 48, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 48
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-48

Query Match      95.3%; Score 2553; DB 1; Length 499;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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15 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 74
 1 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 60
 75 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 134
 61 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 120
 135 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 194
 121 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 180
 195 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 254
 181 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 240
 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314
 241 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 300
 315 WALAEILNPKVLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVKR 374
 301 WALAEILNPKVLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVKR 360
 375 KCTECEINGVYIPGALILFNVMQVGRDPKYWRPSEFRPERFLETGAEAGAPLDLGR 434
 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWRPSEFRPERFLETGAEAGAPLDLGR 420
 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOQILKGGDAKVSMEER 494
 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOQILKGGDAKVSMEER 480
 495 AGLTVPRAHSLVCVPLARI 513
 481 AGLTVPRAHSLVCVPLARI 499
 RESULT 12
 US-09-857-581-18
 ; Sequence 18, Application US/09857581
 ; GENERAL INFORMATION:
 ; APPLICANT: E. I. du Pont de Nemours and Company
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
 ; FILE REFERENCE: BB1339 PCT
 ; CURRENT APPLICATION NUMBER: US/09/857,581
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR FILING DATE: 60/117,769
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR FILING DATE: 60/144,783
 ; PRIOR FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 18
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Vicia villosa
 US-09-857-581-18
 Query Match 95.1%; Score 2548; DB 1; Length 499;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 493; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 15 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 74
 1 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 60
 75 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 134
 61 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 120

135 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 194
 121 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 180
 195 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 254
 181 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 240
 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314
 241 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 300
 315 WALAEILNPKVLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVKR 374
 301 WALAEILNPKVLEKAREEVSVMGKDRLVDEVDTQNLPIYRAIVKETFMRHPPPLPVVKR 360
 375 KCTECEINGVYIPGALILFNVMQVGRDPKYWRPSEFRPERFLETGAEAGAPLDLGR 434
 361 KCTECEINGVYIPGALILFNVMQVGRDPKYWRPSEFRPERFLETGAEAGAPLDLGR 420
 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOQILKGGDAKVSMEER 494
 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFDLQVLGPOQILKGGDAKVSMEER 480
 495 AGLTVPRAHSLVCVPLARI 513
 481 AGLTVPRAHSLVCVPLARI 499
 RESULT 13
 US-09-857-581-55
 ; Sequence 55, Application US/09857581
 ; GENERAL INFORMATION:
 ; APPLICANT: E. I. du Pont de Nemours and Company
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
 ; FILE REFERENCE: BB1339 PCT
 ; CURRENT APPLICATION NUMBER: US/09/857,581
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR FILING DATE: 60/117,769
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR FILING DATE: 60/144,783
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR FILING DATE: 60/156,094
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 55
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Lupinus albus
 US-09-857-581-55
 Query Match 95.0%; Score 2544; DB 1; Length 499;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 493; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 15 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 74
 1 FLHLRPTPTAKSKALRHLNPPSPKPLPFIHLLKDKLLHVALIDLSKKHGPLFSLY 60
 75 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 134
 61 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGPKVFKRL 120
 135 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 194
 121 IMNDLLNATTNKLRLPRTQOIRKFLRVAQAQAQKPLDLTBECLKWTNSTISMMMLGE 180
 195 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 254
 181 ABEIRDIAREVLKIFGEYSYSLDFIWLKHLKVGKYEKRIIDILNKFDVVERVVKRREI 240
 255 VRRRKNGEVGEVSGVFLDTLLFAEDTMEIKITKDHIKGLVVDVDFSSAGTSTAVATE 314


```
RESULT 16
US-09-857-581-61
; Sequence 61, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 61
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-61

Query Match 94.3%; Score 2525; DB 1; Length 498;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 489; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 16 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLFSLYF 75
Db 1 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLFSHYF 60

QY 76 GSMTPVASTTPELFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVKLI 135
Db 61 GSMTPVASTTPELFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVKLI 120

QY 136 MNDLLNATTNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTEELLKWTNSTISMMMLGEA 195
Db 121 MNDLLNATTNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTEELLKWTNSTISMMMLGEA 180

QY 196 BEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREIV 255
Db 181 BEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREIV 240

QY 256 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFPSAGTDSATAVEW 315
Db 241 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFPSAGTDSATAVEW 300

QY 316 ALAELINNPVKLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETPRMHPPLPVVKRK 375
Db 301 ALAELINNPVKLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETPRMHPPLPVVKRK 360

QY 376 CTECEINGYVPEGALIFPNVQVGRDPKYWDRESEFRPFLETGAEGAGPLDLRGQ 435
Db 361 CTECEINGYVPEGALIFPNVQVGRDPKYWDRESEFRPFLETGAEGAGPLDLRGQ 420

QY 436 HFQQLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEERA 495
Db 421 HFQQLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEERA 480

QY 496 GLTVPRASHLVCVPLARI 513
Db 481 GLTVPRASHLVCVPLARI 498
```

```
RESULT 17
US-09-857-581-20
; Sequence 20, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
```

```
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-20

Query Match 94.0%; Score 2519; DB 1; Length 499;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 486; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 15 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLFSLY 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLHYALIDLKSKHGFLFSLY 60

QY 75 FGSMTPVASTTPELFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVKRL 134
Db 61 FGSMTPVASTTPELFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVPFGPYWKFVKRL 120

QY 135 IMNDLLNATTNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTEELLKWTNSTISMMMLGE 194
Db 121 IMNDLLNATTNKLRLPTQOIRKFLRWMAQGAQAQKPLDLTEELLKWTNSTISMMMLGE 180

QY 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 240

QY 255 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFPSAGTDSATAVE 314
Db 241 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKHDKGLVWDFPSAGTDSATAVE 300

QY 315 WALAELINNPVKLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETPRMHPPLPVVKRK 374
Db 301 WALAELINNPVKLEKAREEYISVVGKDLVDEVDTONLPYIRAI VKETPRMHPPLPVVKRK 360

QY 375 KCTECEINGYVPEGALIFPNVQVGRDPKYWDRESEFRPFLETGAEGAGPLDLRG 434
Db 361 KCTECEINGYVPEGALIFPNVQVGRDPKYWDRESEFRPFLETGAEGAGPLDLRG 420

QY 435 QHFQQLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEER 494
Db 421 QHFQQLPFGSGRRMCPGVNLATSGMATLLASLIQCFLQVLGPGQILKGGDAKYSMEER 480

QY 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
```

```
RESULT 18
US-09-857-581-16
; Sequence 16, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
```

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 16

; LENGTH: 499

; TYPE: PRT

; ORGANISM: Medicago sativa

US-09-857-581-16

Query Match

Best Local Similarity 93.2%; Score 2498; DB 1; Length 499;

Matches 481; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```
QY 15 FLHLRPTAKSKALRHLNPPSPKPLPFIHLLHLLKDLKLLHYALIDLSKKGHPFSLY 74
DB 1 FLHLRPTPSAKSKALRHLNPPSPKPLPFIHLLHLLKDLKLLHYALIDLSKKGHPFSL 60
QY 75 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPPGPKVVRKL 134
DB 61 FGSMTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPPGPKVVRKL 120
QY 135 IMNDLLNATTVNKLRLPRTQOIRKFLRVMAQGAEAQKPLDITTELLKWTNSTISMMMLGE 194
DB 121 IMNDLLNATTVNKLRLPRTQOIRKFLRVMAQGAEAQKPLDITTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSLTDFIWP LKYLKVGKYEKRIDDIILNKFPDPVVERVIKKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDFIWP LKYLKVGKYEKRIDDIILNKFPDPVVERVIKKRREI 240
QY 255 VRRKNGEVVEGSGVFLDTLLLEFADETMETIKTKDHIKGLVDPFFSAGTSTAVATE 314
DB 241 VRRKNGEVVEGSGVFLDTLLLEFADETMETIKTKDHIKGLVDPFFSAGTSTAVATE 300
QY 315 WALAELINNPVKLEKAREEYVSVVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKR 374
DB 301 WALAELINNPVKLEKAREEYVSVVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKR 360
QY 375 KCTECCINGVVIPEGALILFNWQVGRDPKYWDRESEPRPERFLETGAEAGEAGPLDLRG 434
DB 361 KCTECCINGVVIPEGALILFNWQVGRDPKYWDRESEPRPERFLETGAEAGEAGPLDLRG 420
QY 435 QHFOFLPFSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSNEER 494
DB 421 QHFOFLPFSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSNEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
```

RESULT 19

US-09-857-581-38

; Sequence 38, Application US/09857581

; GENERAL INFORMATION:

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase

; FILE REFERENCE: B81339 PCT

; CURRENT APPLICATION NUMBER: US/09/857,581

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769

; PRIOR FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: 60/144,783

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 60/156,094

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 38

; TYPE: PRT

; LENGTH: 498

; ORGANISM: Trifolium repens

US-09-857-581-38

Query Match

Best Local Similarity 92.3%; Score 2473; DB 1; Length 498;

Matches 481; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

```
Matches 477; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
QY 17 HLRLPTAKSKALRHLNPPSPKPLPFIHLLHLLKDLKLLHYALIDLSKKGHPFSLYFG 76
DB 2 HLRLPTSAISAKALRHLNPPSPKPLPFIHLLHLLKDLKLLHYALIDLSKKGHPFSLYFG 61
QY 77 SMTPTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPPGPKVVRKLIM 136
DB 62 SMTPTVASTPELFLKFLQTHEATSFNTRFQTSARRLTYDSSVAMVPPGPKVVRKLIM 121
QY 137 NDLLNATTVNKLRLPRTQOIRKFLRVMAQGAEAQKPLDITTELLKWTNSTISMMMLGEAE 196
DB 122 NDLLNATTVNKLRLPRTQOIRKFLRVMAQGAEAQKPLDITTELLKWTNSTISMMMLGEAE 181
QY 197 EIRDIAREVLKIFGEYSLTDFIWP LKYLKVGKYEKRIDDIILNKFPDPVVERVIKKRREIVR 256
DB 182 EIRDIAREVLKIFGEYSLTDFIWP LKYLKVGKYEKRIDDIILNKFPDPVVERVIKKRREIVR 241
QY 257 RKNNGEVVEGSGVFLDTLLLEFADETMETIKTKDHIKGLVDPFFSAGTSTAVATEWA 316
DB 242 RKNNGEVVEGSGVFLDTLLLEFADETMETIKTKDHIKGLVDPFFSAGTSTAVATEWA 301
QY 317 LAELINNPVKLEKAREEYVSVVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRKC 376
DB 302 LAELINNPVKLEKAREEYVSVVGKDRLVDEVDTONLPYIRAI VKETFRMHPPLPVVKRKC 361
QY 377 TEECEINGVVIPEGALILFNWQVGRDPKYWDRESEPRPERFLETGAEAGEAGPLDLRGQH 436
DB 362 TEECEINGVVIPEGALILFNWQVGRDPKYWDRESEPRPERFLETGAEAGEAGPLDLRGQH 421
QY 437 FOLLFPFGSRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSNEERAG 496
DB 422 FOLLFPFGSRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQOILKGGDAKVSNEERAG 481
QY 497 LTVPRAHSLVCVPLARI 513
DB 482 LTVPRAHSLVCVPLARI 498
```

Search completed: March 1, 2004, 07:06:48

Job time : 2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2004, 07:04:37 ; Search time 1 Seconds
(without alignments)
5.031 Million cell updates/sec

Title: af022462pep
Perfect score: 2583
Sequence: 1 MLELALGLLVLFHLP.....AHSILVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 19 seqs, 9656 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ramirez581.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2651	98.8	521	1	US-09-857-581-26
2	2651	98.8	522	1	US-09-857-581-24
3	2649	98.7	521	1	US-09-857-581-28
4	2649	98.7	521	1	US-09-857-581-30
5	2649	98.7	521	1	US-09-857-581-34
6	2636	98.2	521	1	US-09-857-581-32
7	2598	96.8	521	1	US-09-857-581-2
8	2580	95.2	521	1	US-09-857-581-36
9	2547	94.9	499	1	US-09-857-581-59
10	2538	94.6	499	1	US-09-857-581-22
11	2537	94.6	499	1	US-09-857-581-48
12	2532	94.4	499	1	US-09-857-581-18
13	2528	94.2	499	1	US-09-857-581-55
14	2523	94.0	499	1	US-09-857-581-57
15	2512	93.6	499	1	US-09-857-581-40
16	2509	93.5	498	1	US-09-857-581-61
17	2503	93.3	499	1	US-09-857-581-20
18	2482	92.5	499	1	US-09-857-581-16
19	2457	91.6	498	1	US-09-857-581-38

ALIGNMENTS

RESULT 1
US-09-857-581-26
; Sequence 26, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-26

Query Match 98.8%; Score 2651; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLELALGLLVLFHLPPTAKSKALRHLPNPPSPKRLPFFIGHLHLLKDLHYAL 60
DB 1 MLELALGLLVLFHLPPTAKSKALRHLPNPPSPKRLPFFIGHLHLLKDLHYAL 60

QY 61 IDLSKKGHPFLSYFGSMPTVAVSTPELPKLPLOTHEATSFNTRPOTSAIRRLTYDSSVA 120
DB 61 IDLSKKGHPFLSYFGSMPTVAVSTPELPKLPLOTHEATSFNTRPOTSAIRRLTYDSSVA 120

QY 121 MYPFGPYWKFVKLIWMDLPNATTVNKLRLPRTQOTRFLRWAOCAQAQKPLDLTEELL 180
DB 121 MYPFGPYWKFVKLIWMDLPNATTVNKLRLPRTQOTRFLRWAOCAQAQKPLDLTEELL 180

QY 181 KWTNSTISMMILGEAEIRDIAREVLKIPGEVSLTDFIWPMLKLVKGVKKEIDILNKF 240
DB 181 KWTNSTISMMILGEAEIRDIAREVLKIPGEVSLTDFIWPMLKLVKGVKKEIDILNKF 240

QY 241 DPVVERVIKRRREIVRRKNGEVSGVGLDITLLEPADETEIKITKHIGLVVD 300
DB 241 DPVVERVIKRRREIVRRKNGEVSGVGLDITLLEPADETEIKITKHIGLVVD 300

QY 301 FFSAGTSDTAVATEWALAEILNPNKVKLEKAREEVSVVGKRLVDEVDTONLPYIRAIYK 360
DB 301 FFSAGTSDTAVATEWALAEILNPNKVKLEKAREEVSVVGKRLVDEVDTONLPYIRAIYK 360

QY 361 EFRMHPPVPPVKKKCTEECEINGVYIPGAILFNWGVGDPKYWDPSFRFRERFLE 420
DB 361 EFRMHPPVPPVKKKCTEECEINGVYIPGAILFNWGVGDPKYWDPSFRFRERFLE 420

QY 421 TGAEGAGPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQG 480
DB 421 TGAEGAGPLDLRGQHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLGPOQG 480

QY 481 ILKGGDAKVMEEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
DB 481 ILKGGDAKVMEEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 2
US-09-857-581-24
; Sequence 24, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-24

Query Match      98.8%; Score 2651; DB 1; Length 522;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60
Db 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60

Qy 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180

Qy 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSITDFTWPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGEABEIRDIAREVLKIFGEYSITDFTWPLKHLKVGKYEKRIDDILNKF 240

Qy 241 DPWVERVIKGRREIVRRKNGEVEGVSFVLDLLEFADETMETIKITKDHIEGLVVD 300
Db 241 DPWVERVIKGRREIVRRKNGEVEGVSFVLDLLEFADETMETIKITKDHIEGLVVD 300

Qy 301 PFSAGTDSATAVATEWALAEELNNPKVLEKAREEVSUVGKDRLVDEVDTONLPYIRAIK 360
Db 301 PFSAGTDSATAVATEWALAEELNNPKVLEKAREEVSUVGKDRLVDEVDTONLPYIRAIK 360

Qy 361 ETRFMHPPLPVVKRKTCECEINGYVPEGALILFNVMQVGRDPKYMDRPSSEPRPERFLE 420
Db 361 ETRFMHPPLPVVKRKTCECEINGYVPEGALILFNVMQVGRDPKYMDRPSSEPRPERFLE 420

Qy 421 TGAEGEAGPLDLRGHQLFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPGQG 480
Db 421 TGAEGEAGPLDLRGHQLFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPGQG 480

Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 4
US-09-857-581-30
; Sequence 30, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; TYPE: PRT
; ORGANISM: Phaseolus aureus
US-09-857-581-30

Query Match      98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60
Db 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60

Qy 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180

Query Match      98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60
Db 1 MLELALGLLVLAFLHLRPTPTAKSKALRHLNPPSPKRLPFIFGHLHLKDKLHYAL 60

Qy 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPLSLYFGSMPTVASTPELFLKFLQTHEATSFNTRFQTSAIRRLTYDSSVA 120

Qy 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180
Db 121 MYPFGPYWKFKVRKLIIMNDLPNATTNKNLRLPTQOTRKFLEVMQAQGAQKPLDLTEELL 180
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Db 121 MPPGPGYKFKVRKLIIMNDLLNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDLVLPQGG 480
Db 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDLVLPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 5
US-09-857-581-34
; Sequence 34, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-34

Query Match 98.7%; Score 2649; DB 1; Length 521;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 516; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKOKLLHYAL 60
Db 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKOKLLHYAL 60
Qy 61 IDLSKKGHPLSLYFGSMPTVASTPELFLQTHATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPLSLYFGSMPTVASTPELFLQTHATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Db 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
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Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Qy 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDLVLPQGG 480
Db 421 TGAGEAGPLDLRGQHQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDLVLPQGG 480
Qy 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 6
US-09-857-581-32
; Sequence 32, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 32
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Trifolium pratense
US-09-857-581-32

Query Match 98.2%; Score 2636; DB 1; Length 521;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 514; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKOKLLHYAL 60
Db 1 MLELALGLLVALLFLHLRPTTAKSKALRHLNPPSPKPLPFIHGLHLKOKLLHYAL 60
Qy 61 IDLSKKGHPLSLYFGSMPTVASTPELFLQTHATSFNTRFQTSAIRRLTYDSSVA 120
Db 61 IDLSKKGHPLSLYFGSMPTVASTPELFLQTHATSFNTRFQTSAIRRLTYDSSVA 120
Qy 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Db 121 MPPGPGYKFKVRKLIIMNDLPNATTNVNKLRLTQIRKFLRVMAQGAQKPLDLTEELL 180
Qy 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Db 181 KWTNSTISMMMLGABEIRDIAREVLKIFGEYSLTDFIWLPLKHLKVGKYEKRIDDILNKF 240
Qy 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Db 241 DPVVERVIKKREIVRRKNGEVGEVSGVFLDTLLEFAEDETMEIKITKDHIEGLVVD 300
Qy 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Db 301 FFSAGTDSATAVATEWALAELINNPVKLEKAREEYVSVGKDRLVDEVDTQNLPIYIRAIK 360
Qy 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
Db 361 ETRFMHPPLPVVKRCKTECEINGYVPEGALILFNVMQVGRDPKYWDRPSEFRPERFLE 420
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QY 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
Db 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 7
US-09-857-581-2
; Sequence 2, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-09-857-581-2

Query Match 96.8%; Score 2598; DB 1; Length 521;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 504; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 1 MLELALGLLVLTALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYAL 60
Db 1 MLELALGLFVLALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYAL 60
QY 61 IDLSKXHGPLFSLYFGSGMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGPLFSLYFGSGMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
QY 121 MYPFGPYKFKVRLINNDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
Db 121 MYPFGPYKFKVRLINNDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
QY 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIIDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIIDILNKF 240
QY 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLEFAEDTMEIKITKHIEGLVVD 300
Db 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLEFAEDTMEIKITKHIEGLVVD 300
QY 301 FFSAGTDSATAWALAEILNNPKVLEKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAWALAEILNNPKVLEKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
QY 361 ETRFMHPPLPVVKRKCTECEINGYVPEGALILFNVQVGRDPKYWDRPSFRPERFLE 420
Db 361 ETRFMHPPLPVVKRKCTECEINGYVPEGALILFNVQVGRDPKYWDRPSFRPERFLE 420
QY 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
Db 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 8
US-09-857-581-36
; Sequence 36, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 36
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-857-581-36
Query Match 96.2%; Score 2580; DB 1; Length 521;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 499; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MLELALGLLVLTALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYAL 60
Db 1 MLELALGLFVLALFLHLRPTPTAKSKALRHLPNPPSPKPLPFIHGLHLLKDKLLHYAL 60
QY 61 IDLSKXHGPLFSLYFGSGMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
Db 61 IDLSKXHGPLFSLYFGSGMPTVASTPELFLQTHAETSNTFRQTSAIRRLTYDSSVA 120
QY 121 MYPFGPYKFKVRLINNDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
Db 121 MYPFGPYKFKVRLINNDLNNATTNNKLRPLRTOQIRKFLRMAQSAQAQKPLDVTBELL 180
QY 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIIDILNKF 240
Db 181 KWTNSTISMMMLGEAEIRDIAREVLKIFGEVSLTDFIWLKHLKVGKYEKRIIDILNKF 240
QY 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLEFAEDTMEIKITKHIEGLVVD 300
Db 241 DPVVERVVKRREIVRRRNKNGEVGSGVFLDTLLEFAEDTMEIKITKHIEGLVVD 300
QY 301 FFSAGTDSATAWALAEILNNPKVLEKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
Db 301 FFSAGTDSATAWALAEILNNPKVLEKAREEVSVVGVKDRLVDEVDTONLPYIRAIK 360
QY 361 ETRFMHPPLPVVKRKCTECEINGYVPEGALILFNVQVGRDPKYWDRPSFRPERFLE 420
Db 361 ETRFMHPPLPVVKRKCTECEINGYVPEGALILFNVQVGRDPKYWDRPSFRPERFLE 420
QY 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
Db 421 TGAEGAGPLDLRGQHFLQFLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLDQVLGPQG 480
QY 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521
Db 481 ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS 521

RESULT 9
US-09-857-581-59
; Sequence 59, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581

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; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-59

Query Match
Best Local Similarity 94.9%; Score 2547; DB 1; Length 499;
Matches 492; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 15 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLLHYALIDLSKKGGLPFSLY 74
DB 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLKDKLLHYALIDLSKKGGLPFSLY 60
QY 75 FGSMTTVAASPELFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 134
DB 61 FGSMTTVAASPELFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPFGPYKFKVRKL 120
QY 135 IMNDLPNATTNKLRLPTQOTRKFLRVMAQGAQAQKPLDLTEELLKWTNSTISMMLGE 194
DB 121 IMNDLPNATTNKLRLPTQOTRKFLRVMAQGAQAQKPLDLTEELLKWTNSTISMMLGE 180
QY 195 ABEIRDIAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 254
DB 181 ABEIRDIAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIIDILNKFPDPVVERVVKRREI 240
QY 255 VRRXKNGEVVEGSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDFFSAGTSTAVATE 314
DB 241 VRRXKNGEVVEGSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDFFSAGTSTAVATE 300
QY 315 WALAELINNPVKLEKAREEVSVVGKDLRVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 374
DB 301 WALAELINNPVKLEKAREEVSVVGKDLRVDEVDTONLPYIRAIKVTFRMHPPPLPVVKR 360
QY 375 KCTECEINGYVIPGALLIFNVQVGRDPKYWDPRSPFRPERFLETGAEGEAGPLDLRG 434
DB 361 KCTECEINGYVIPGALLIFNVQVGRDPKYWDPRSPFRPERFLETGAEGEAGPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPGQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFDLQVLGPGQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499

RESULT 10
US-09-857-581-22
; Sequence 22, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 59
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-48

Query Match
Best Local Similarity 94.6%; Score 2537; DB 1; Length 499;
Matches 492; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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QY 15 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 60
QY 75 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 300
QY 315 WALAEILNNPKVLEKAREEVSIVGKRLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR 374
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 254
QY 255 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 300
QY 315 WALAEILNNPKVLEKAREEVSIVGKRLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR 374
DB 301 WALAEILNNPKVLEKAREEVSIVGKRLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR 360
QY 375 KCTECEINGYVPEGAILFNWQVGRDPKYWDPSFRPERFLETGAEGEARPLDLRG 434
DB 361 KCTECEINGYVPEGAILFNWQVGRDPKYWDPSFRPERFLETGAEGEARPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
RESULT 12
US-09-857-581-18
; Sequence 18, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Vicia villosa
US-09-857-581-18
Query Match 94.4%; Score 2532; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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QY 15 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 60
QY 75 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
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QY 135 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 314
DB 241 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 300
QY 315 WALAEILNNPKVLEKAREEVSIVGKRLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR 374
DB 301 WALAEILNNPKVLEKAREEVSIVGKRLVDEVDTONLPYIRAIKVFTRMHPPLPVVVKR 360
QY 375 KCTECEINGYVPEGAILFNWQVGRDPKYWDPSFRPERFLETGAEGEARPLDLRG 434
DB 361 KCTECEINGYVPEGAILFNWQVGRDPKYWDPSFRPERFLETGAEGEARPLDLRG 420
QY 435 QHFQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 494
DB 421 QHFQLLPFGSGRRMCPGVNLTATSGMATLLASLIQCFLQVLGPOQIILKGGDAKYSMEER 480
QY 495 AGLTVPRAHSLVCVPLARI 513
DB 481 AGLTVPRAHSLVCVPLARI 499
RESULT 13
US-09-857-581-55
; Sequence 55, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 55
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lupinus albus
US-09-857-581-55
Query Match 94.2%; Score 2528; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
```

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QY 15 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 74
DB 1 FLHRLPTAKSKALRHLPNPPSPKRLPFIHGLHLLKOKLLHYALIDLSKKHGPLFSLY 60
QY 75 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 134
DB 61 FGSMPVTVAASPPELFXFLQTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYPWKFVRKL 120
QY 135 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 194
DB 121 IMNDLPNATTNNKLRPLRTQOTKFLRVMAQGAQAQKPLDTELLKWTNSTISMMMLGE 180
QY 195 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 254
DB 181 ABEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIIDILANKFDPVVERVIKRRREI 240
QY 255 VRRKNGEVEGEVSGVFLDTLLEFAEDTMEIKITKDHIEGLVVDVDFPSAGTSTAVATE 314
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Db 241 VRRKNGEVEGEVSGVLLDTLLEFADETEWEIKTKDHKGLVDFFSAGTDSAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 14
US-09-857-581-57
; Sequence 57, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 57
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-857-581-57

Query Match 94.0%; Score 2523; DB 1; Length 499;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 490; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 15 FLHLRPTTAKSKALRHLNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKHGPLPSLY 74
Db 1 FLHLRPTTAKSKALRHLNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKHGPLPSLY 60
Qy 75 FGSMTVVASTPELPFKLFLOTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYWKFVRKL 134
Db 61 FGSMTVVASTPELPFKLFLOTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYWKFVRKL 120
Qy 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQPLDLTBECLKWTNSTISMMMLGE 194
Db 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQPLDLTBECLKWTNSTISMMMLGE 180
Qy 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVIKGRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVIKGRREI 240
Qy 255 VRRKNGEVEGEVSGVFLDTLLEFADETEWEIKTKDHIEGLVDFFSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLEFADETEWEIKTKDHIEGLVDFFSAGTDSAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
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Db 361 KCTECEINGVVIPEGALILFNVMQVGRDSKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499

RESULT 15
US-09-857-581-40
; Sequence 40, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BBI339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Trifolium repens
US-09-857-581-40

Query Match 93.6%; Score 2512; DB 1; Length 499;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 484; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 15 FLHLRPTTAKSKALRHLNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKHGPLPSLY 74
Db 1 FLHLRPTTAKSKALRHLNPPSPKPRLPFFIGHLLHLLKDLHYALIDLSKKHGPLPSLY 60
Qy 75 FGSMTVVASTPELPFKLFLOTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYWKFVRKL 134
Db 61 FGSMTVVASTPELPFKLFLOTHEATSFNTRFQTSAIRRLTYDSSVAMVPPGYWKFVRKL 120
Qy 135 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQPLDLTBECLKWTNSTISMMMLGE 194
Db 121 IMNDLPNATTNKLRLPRTQOTRKFRLVMAQGAQAQPLDLTBECLKWTNSTISMMMLGE 180
Qy 195 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVIKGRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPVVERVIKGRREI 240
Qy 255 VRRKNGEVEGEVSGVFLDTLLEFADETEWEIKTKDHIEGLVDFFSAGTDSAVATE 314
Db 241 VRRKNGEVEGEVSGVFLDTLLEFADETEWEIKTKDHIEGLVDFFSAGTDSAVATE 300
Qy 315 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 374
Db 301 WALAELINNNKVLKAREEYVSVGKDRLVDEVDTONLPYIRAIKVFEMHPLPVVVKR 360
Qy 375 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 434
Db 361 KCTECEINGVVIPEGALILFNVMQVGRDPKYWDPSFPRFLETGAEGEAGPLDLRG 420
Qy 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLQVLPQGOQILKGGDAKVSMEER 480
Qy 495 AGLTVPRAHSLVCVPLARI 513
Db 481 AGLTVPRAHSLVCVPLARI 499
```

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RESULT 16
US-09-857-581-61
; Sequence 61, Application: US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 61
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-857-581-61

Query Match      93.5%; Score 2509; DB 1; Length 498;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 486; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 16 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLKSKHGFLFSLYF 75
Db 1 LHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLKSKHGFLFSHYF 60

Qy 76 GSMTPVAVASTPELFLKFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVFFGYWKFVRKLI 135
Db 61 GSMTPVAVASTPELFLKFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVFFGYWKFVRKLI 120

Qy 136 MNDLPNATTNKLRLPTQOTRKFLRVMAQGAQKPLDLTEELLKWTNSTISMMMLGEA 195
Db 121 MNDLLNATTNKLRLPTQOTRKFLRVMAQGAQKPLDLTEELLKWTNSTISMMMLGEA 180

Qy 196 EBIROIAREVLKIFGEYSLTDIFWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREIV 255
Db 181 EBIROIAREVLKIFGEYSLTDIFWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREIV 240

Qy 256 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSATAVEW 315
Db 241 RRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSATAVEW 300

Qy 316 ALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKRK 375
Db 301 ALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKRK 360

Qy 376 CTEECINGYVTPGALILFNWQVGRDPKYWDRESEPRPERFLETGAEGAGPLDLRGQ 435
Db 361 CTEECINGYVTPGALILFNWQVGRDPKYWDRESEPRPERFLETGAEGAGPLDLRGQ 420

Qy 436 HFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEERA 495
Db 421 HFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEERA 480

Qy 496 GLTVBRAHSLVCVPLARI 513
Db 481 GLTVBRAHSLVCVPLARI 498

RESULT 17
US-09-857-581-20
; Sequence 20, Application: US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
```

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; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Lens culinaris
US-09-857-581-20

Query Match      93.3%; Score 2503; DB 1; Length 499;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 483; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 15 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLKSKHGFLFSLY 74
Db 1 FLHLRPTTAKSKALRHLPNPPSPKPRLPFFIGHLLHLLKDLHYALIDLKSKHGFLFSLY 60

Qy 75 FGSMTPVAVASTPELFLKFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVFFGYWKFVRKL 134
Db 61 FGSMTPVAVASTPELFLKFLQTHAETSFNTRFQTSAIRRLTYDSSVAMVFFGYWKFVRKL 120

Qy 135 MNDLPNATTNKLRLPTQOTRKFLRVMAQGAQKPLDLTEELLKWTNSTISMMMLGE 194
Db 121 MNDLLNATTNKLRLPTQOTRKFLRVMAQGAQKPLDLTEELLKWTNSTISMMMLGE 180

Qy 195 ABEIRDIAREVLKIFGEYSLTDIFWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREI 254
Db 181 ABEIRDIAREVLKIFGEYSLTDIFWPLKHLKVGKYEKRIDDILNKFPDPVVERVVKRRREI 240

Qy 255 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSATAVE 314
Db 241 VRRKNGEVVEGVSQVFLDTLLEFAEDTMEIKTKDHIEGLVVDFFSAGTDSATAVE 300

Qy 315 WALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKR 374
Db 301 WALAEELNNPKVLEKAREEYISVVGKDRLVDEVDTONLPYIRAIKVTFRMHPPLPVVKR 360

Qy 375 KCTEECEINGYVTPGALILFNWQVGRDPKYWDRESEPRPERFLETGAEGAGPLDLRG 434
Db 361 KCTEECEINGYVTPGALILFNWQVGRDPKYWDRESEPRPERFLETGAEGAGPLDLRG 420

Qy 435 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEER 494
Db 421 QHFQLLPFGSGRRMCPGVNLTSGMATLLASLIQCFLDQVLGPGQILKGGDAKYSMEER 480

Qy 495 AGLTVBRAHSLVCVPLARI 513
Db 481 AGLTVBRAHSLVCVPLARI 499

RESULT 18
US-09-857-581-16
; Sequence 16, Application: US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
```

SOFTWARE: Microsoft Office 97
SEQ ID NO 15
Best Local Similarity 95.8%; Pred. No. 0;
Matches 478; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
TYPE: PRT
ORGANISM: Medicago sativa
US-09-857-581-16

Query Match 92.5%; Score 2482; DB 1; Length 499;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 478; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy	15	FLHLRPTAKSKALRHLNPPSPKRLPPIGHLHLKDLHYALIDLSKKGPLFSLY	74
Db	1	FLHLRPTAKSKALRHLNPPSPKRLPPIGHLHLKDLHYALIDLSKKGPLFSLS	60
Qy	75	FGSMFTVASTPELFLQTHATSNTFRFQTSAIRRLTYDSSVAMVPPGPKVVRKL	134
Db	61	FGSMFTVASTPELFLQTHATSNTFRFQTSAIRRLTYDSSVAMVPPGPKVVRKL	120
Qy	135	IMNDLPNATTNKLRLPRTQOTRKFLRVMAQGAQAOKPLDLTEELLKWTNSTISMMMLGE	194
Db	121	IMNDLPNATTNKLRLPRTQOTRKFLRVMAQGAQAOKPLDLTEELLKWTNSTISMMMLGE	180
Qy	195	AEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPDPPVVERVVKRRREI	254
Db	181	AEIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPDPPVVERVVKRRREI	240
Qy	255	VRKNGEVVEGEVSGVFLDTLLEFADETMETIKITKHIEGLVVDFFSAGTSDTAVATE	314
Db	241	VRKNGEVVEGEVSGVFLDTLLEFADETMETIKITKHIEGLVVDFFSAGTSDTAVATE	300
Qy	315	WALAEILNNPKVLEKAREEVYVVGKDRLVDEVDTONLPIRAIVKETFPMHPPPLPVVKR	374
Db	301	WALAEILNNPKVLEKAREEVYVVGKDRLVDEVDTONLPIRAIVKETFPMHPPPLPVVKR	360
Qy	375	KCTEECEINGVIPEGALILFNWQVGRDPKYWDPSERPERFLETGAEGAGPLDLRG	434
Db	361	KCTEECEINGVIPEGALILFNWQVGRDPKYWDPSERPERFLETGAEGAGPLDLRG	420
Qy	435	QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPGQQLKGGDAKVSMEER	494
Db	421	QHFQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPGQQLKGGDAKVSMEER	480
Qy	495	AGLTVPRAHSLVCVPLARI	513
Db	481	AGLTVPRAHSLVCVPLARI	499

RESULT 19
US-09-857-581-38
Sequence 38, Application US/09857581
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
FILE REFERENCE: BE1339 PCT
CURRENT APPLICATION NUMBER: US/09/857,581
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/117,769
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/144,783
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/156,094
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Microsoft Office 97
SEQ ID NO 38
LENGTH: 498
TYPE: PRT
ORGANISM: Trifolium repens
US-09-857-581-38

Query Match 91.6%; Score 2457; DB 1; Length 498;
Best Local Similarity 95.4%; Pred. No. 0;

Matches	474;	Conservative	11;	Mismatches	12;	Indels	0;	Gaps	0;
Qy	17	HLRPTAKSKALRHLNPPSPKRLPPIGHLHLKDLHYALIDLSKKGPLFSLYFG	76						
Db	2	HLRPTAKSKALRHLNPPSPKRLPPIGHLHLKDLHYALIDLSKKGPLFSLYFG	61						
Qy	77	SMPTVASTPELFLQTHATSNTFRFQTSAIRRLTYDSSVAMVPPGPKVVRKLIM	136						
Db	62	SMPTVASTPELFLQTHATSNTFRFQTSAIRRLTYDSSVAMVPPGPKVVRKLIM	121						
Qy	137	NDLPNATTNKLRLPRTQOTRKFLRVMAQGAQAOKPLDLTEELLKWTNSTISMMMLGEAE	196						
Db	122	NDLPNATTNKLRLPRTQOTRKFLRVMAQGAQAOKPLDLTEELLKWTNSTISMMMLGEAE	181						
Qy	197	EIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPDPPVVERVVKRRREIVR	256						
Db	182	EIRDIAREVLIKIFGEYSLTDFIWLKHLKVGKYEKRIDDILNKFPDPPVVERVVKRRREIVR	241						
Qy	257	RRKNGEVVEGEVSGVFLDTLLEFADETMETIKITKHIEGLVVDFFSAGTSDTAVATEWA	316						
Db	242	RRKNGEVVEGEVSGVFLDTLLEFADETMETIKITKHIEGLVVDFFSAGTSDTAVATEWA	301						
Qy	317	LAELINNPKVLEKAREEVYVVGKDRLVDEVDTONLPIRAIVKETFPMHPPPLPVVKRKC	376						
Db	302	LAELINNPKVLEKAREEVYVVGKDRLVDEVDTONLPIRAIVKETFPMHPPPLPVVKRKC	361						
Qy	377	TEECINGVIPEGALILFNWQVGRDPKYWDPSERPERFLETGAEGAGPLDLRGQH	436						
Db	362	TEECINGVIPEGALILFNWQVGRDPKYWDPSERPERFLETGAEGAGPLDLRGQH	421						
Qy	437	FQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPGQQLKGGDAKVSMEERAG	496						
Db	422	FQLLPFGSGRRMCPGVNLATSGMATLLASLIQCFLDQVLGPGQQLKGGDAKVSMEERAG	481						
Qy	497	LTVPRAHSLVCVPLARI	513						
Db	482	LTVPRAHSLVCVPLARI	498						

Search completed: March 1, 2004, 07:04:40
Job time : 3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2004, 16:55:28 : Search time 1 Seconds
(without alignments)

Title: AF022462

Perfect score: 1824

Sequence: 1 GGAAATTAGCCTCACAAA.....TAAACTATCAATCCTTATAT 1824

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1 segs. 1722 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq	length: 2000000000
Maximum DB seq	length: 2000000000

Faintly

Post-processing: Minimum Match 0%

Listing first 1 summaries

Database : af135484.gb pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1685.9	92.4	1722	1	AF135484	ACCESSION:AF135484

ALIGNMENTS

[illegible]

KEYWORDS
SOURCE
Glycine max (soybean)

LOOKUP	GLYCINE max	GLYCINE max (boydian)
ORGANISM	GLYCINE max	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 1722)
GLYCINE.

REFERENCE
I (Pases I CO 1722)
AUTHORS
Steele C. I., Gizen M., Outob. D. and Dixon B. A.

<p>AUTHORS</p> <p>steere, C. L.; Gijzen, M.; Quoad, D.; and Dixon, R. A.</p>	<p>TITLE</p> <p>Molecular characterization of the enzyme catalyzing the aryl</p>
---	---

migration reaction of isoflavonoid biosynthesis in soybean

JOURNAL
Arch. Bio-

MEDLINE 99306846

PUBMED 10375412

REFERENCE 2 (bases 1 to 172)

AUTHORS Steele, C.L., Gijzen, M., Qutob, D. and Dixon, R.A.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam

Noble Pkwy, Ardmore, OK 73402, USA

FEATURES


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QY 380 CATAAGACCCCTCACCTATGATAGCTAGCTGAGTGGCCATGTTCCCTTCGACCTTACTTGAA 439
Db 362 CATAAGACCCCTCACCTATGATAGCTAGCTGAGTGGCCATGTTCCCTTCGACCTTACTTGAA 421
QY 440 GTTCGTGAGGAAGCTCATCATGAACGACCTTCCCAACGCCACCACTGTAAACAAGTTGAG 499
Db 422 GTTCGTGAGGAAGCTCATCATGAACGACCTTCTCAACGCCACCACTGTAAACAAGTTGAG 481
QY 500 GCCTTTGAGGACCCAAACAGACCCGCGAAGTTCCTTAGGGTTATGGCCCAAGGCGCAGAGGC 559
Db 482 GCCTTTGAGGACCCAAACAGATCCGCAAGTTCCTTAGGGTTATGGCCCAAGGCGCAGAGGC 541
QY 560 ACAGAAGCCCTTGACTTACCGAGGAGCTTCTGAATAAGCAACAGCAGCACCATCTCCAT 619
Db 542 ACAGAAGCCCTTGACTTACCGAGGAGCTTCTGAATAAGCAACAGCAGCACCATCTCCAT 601
QY 620 GATGATGCTCGGCGAGGCTGAGGAGATCAGAGACATCGCTCGGAGGTTCTTAAGATCTT 679
Db 602 GATGATGCTCGGCGAGGCTGAGGAGATCAGAGACATCGCTCGGAGGTTCTTAAGATCTT 661
QY 680 TGGCGAATACAGCTCAGCTTCACTGATCTGATGCGCATTAAGCATCTCAAGGTTGGAAGTA 739
Db 662 TGGCGAATACAGCTCAGCTTCACTGATCTGATGCGCATTAAGCATCTCAAGGTTGGAAGTA 721
QY 740 TGAGAAGAGGATCGACGACATCTTGAACAAGTTCGACCTGTCGTTGAAAGGTCATCAA 799
Db 722 TGAGAAGAGGATCGACGACATCTTGAACAAGTTCGACCTGTCGTTGAAAGGTCATCAA 781
QY 800 GAAGCCCGTGAGATCGTGAGGAGGAGAAAGAACCGAGAGGTTGTTGAGGGTGAGGTGAG 859
Db 782 GAAGCCCGTGAGATCGTGAGGAGGAGAAAGAACCGAGAGGTTGTTGAGGGTGAGGTGAG 841
QY 860 CGGGGTTTCCTTGACACTTTCGTTGAATTCGCTGAGGATGAGACCATGGAGATCAAAAT 919
Db 842 CGGGGTTTCCTTGACACTTTCGTTGAATTCGCTGAGGATGAGACCATGGAGATCAAAAT 901
QY 920 CACCAAGGACCAATCGAGGTCCTGTCGACCTTTCTCGGAGGAAACAGACTCCAC 979
Db 902 CACCAAGGACCAATCAAGGTCCTGTCGACCTTTCTCGGAGGAAACAGACTCCAC 961
QY 980 AGCGGTGGCAACAGAGTGGGCTTGGCAGAACTCATCAACATCTTACGTTGGAATA 1039
Db 962 AGCGGTGGCAACAGAGTGGGCTTGGCAGAACTCATCAACATCTTACGTTGGAATA 1021
QY 1040 GGCTCGTGAGGAGGCTTACAGTGTTCGGGAAGGACAGACTTGGACGAAGTTGACAC 1099
Db 1022 GGCTCGTGAGGAGGCTTACAGTGTTCGGGAAGGACAGACTTGGACGAAGTTGACAC 1081
QY 1100 TGAACACCTTCCTTACATTAAGCAATCGTGAAGGAGACTTCCGATGACCCGCCACT 1159
Db 1082 TGAACACCTTCCTTACATTAAGCAATCGTGAAGGAGACTTCCGATGACCCGCCACT 1141
QY 1160 CCCAGTGGTCAAAAGAAAGTGACAGAGTGTGAGATTAATGATATGATGCCAGA 1219
Db 1142 CCCAGTGGTCAAAAGAAAGTGACAGAGTGTGAGATTAATGATATGATGCCAGA 1201
QY 1220 GGGAGCATTAATTCCTTCAATGTATGGCAAGTAGGAAGAGACCCCAATACTGGGACAG 1279
Db 1202 GGGAGCATTAATTCCTTCAATGTATGGCAAGTAGGAAGAGACCCCAATACTGGGACAG 1261
QY 1280 ACCATCGGAGTTCGCTGAGAGGTTCTTAGAGCAGGGGCTGAAGGGGAAGCAGGGCC 1339
Db 1262 ACCATCGGAGTTCGCTGAGAGGTTCTTAGAGCAGGGGCTGAAGGGGAAGCAGGGCC 1321
QY 1340 TCTTGATCTTGGGGAACAATTTCACTTCTCCATTTGGGCTCTGGAGGAGAAATGTG 1399
Db 1322 TCTTGATCTTGGGGAACAATTTCACTTCTCCATTTGGGCTCTGGAGGAGAAATGTG 1381
QY 1400 CCTGGAGTCAATCTCGCTACTTGGGGAATGGCAACACTTCTTGATCTCTTATTACGTG 1459
Db 1382 CCTGGAGTCAATCTCGCTACTTGGGGAATGGCAACACTTCTTGATCTCTTATTACGTG 1441
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QY 1460 CTTTCGACTTTCGCAAGTGTGCTGGTCCCAAGGACAGATATTGAAGGTTGGTGACGCCAAAGT 1519
Db 1442 CTTTCGACTTTCGCAAGTGTGCTGGTCCCAAGGACAGATATTGAAGGTTGGTGACGCCAAAGT 1501
QY 1520 TAGCATGGAAGAGAGAGCGGCTCACTGTTCGAAGGACACATAGTCTTGTCTGTGTTCC 1579
Db 1502 TAGCATGGAAGAGAGAGCGGCTCACTGTTCGAAGGACACATAGTCTTGTCTGTGTTCC 1561
QY 1580 ACTTGCAAGGATCGGCGTTGCACTCTAAACTCCTTTCTTAATTAAAG-----ATCATC 1630
Db 1562 ACTTGCAAGGATCGGCGTTGCACTCTAAACTCCTTTCTTAATTAAAGATCATCGTCATCATC 1621
QY 1631 ATCATATATAATATTTACTTTTTTGTGTGTTGATAATCATCATTTCAATAAGGTTCTGTTTC 1690
Db 1622 ATCATATATAATATTTACTTTTTTGTGTGTTGATAATCATCATTTCAATAAGGTTCTGTTTC 1681
QY 1691 ATCTACTTTTTATCAAGTATATAAGCCCTTCCATGCA 1729
Db 1682 ATCTACTTTTTATCAAGTATATAAGCCCTTCCATGCAAA 1720
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Search completed: February 26, 2004, 16:55:31
Job time : 2 secs